GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 17:23:48 ; Search time 62 Seconds
(without alignments)
1338.972 Million cell updates/sec

Perfect score: 1102
Sequence: 1 MLWLLFFLVTAIHAELCQPG.....ENGIPSDPLDMKGGILMMPS 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
27	1102	100.0	212	10	US-09-997-428-387	Sequence 387, App
515	1102	100.0	212	17	US-10-931-886-482	Sequence 482, App
517	1102	100.0	212	18	US-10-955-952-482	Sequence 482, App
518	1073	97.4	222	14	US-10-097-065-141	Sequence 141, App
519	1073	97.4	222	15	US-10-372-876-141	Sequence 141, App
520	1066	96.7	222	10	US-09-948-783-129	Sequence 129, App
521	1066	96.7	223	10	US-09-892-877-128	Sequence 128, App
522	663	60.2	176	14	US-10-097-065-274	Sequence 274, App
523	663	60.2	176	15	US-10-372-876-274	Sequence 274, App
524	415	37.7	105	14	US-10-097-065-246	Sequence 246, App
525	415	37.7	105	15	US-10-372-876-246	Sequence 246, App
526	376	34.1	805	9	US-09-978-385-2	Sequence 2, Appli
527	376	34.1	805	11	US-09-999-781-2	Sequence 2, Appli
528	376	34.1	805	13	US-10-114-893-86	Sequence 86, Appl
529	376	34.1	805	14	US-10-158-847-142	Sequence 142, App
530	376	34.1	805	14	US-10-005-956-570	Sequence 570, App
531	376	34.1	805	14	US-10-005-956-843	Sequence 843, App
532	376	34.1	805	14	US-10-158-825-142	Sequence 142, App
533	376	34.1	805	16	US-10-158-825-142	Sequence 142, App
534	376	34.1	805	20	US-11-059-218-2	Sequence 2, Appli
535	376	34.1	805	20	US-11-059-218-106	Sequence 106, App
536	361	32.8	805	9	US-09-978-385-6	Sequence 6, Appli
537	361	32.8	805	9	US-09-978-385-9	Sequence 9, Appli
538	359	32.6	711	9	US-09-969-384-13	Sequence 13, Appl
539	359	32.6	711	14	US-10-158-847-138	Sequence 138, App
540	359	32.6	711	14	US-10-158-825-138	Sequence 138, App
541	359	32.6	711	16	US-10-158-825-138	Sequence 138, App
542	330	29.9	64	9	US-09-864-761-39999	Sequence 39999, A
543	289	26.2	681	9	US-09-969-384-25	Sequence 25, Appl
544	289	26.2	681	14	US-10-158-847-140	Sequence 140, App
545	289	26.2	681	14	US-10-158-825-140	Sequence 140, App
546	289	26.2	681	16	US-10-158-825-140	Sequence 140, App
547	133	12.1	24	14	US-10-097-065-277	Sequence 277, App
548	133	12.1	24	15	US-10-372-876-277	Sequence 277, App
549	117	10.6	23	14	US-10-097-065-276	Sequence 276, App
550	117	10.6	23	15	US-10-372-876-276	Sequence 276, App
551	91.5	8.3	545	10	US-09-866-050A-500	Sequence 500, App
552	91.5	8.3	688	10	US-09-866-050A-624	Sequence 624, App
553	90	8.2	25	14	US-10-097-065-275	Sequence 275, App
554	90	8.2	25	15	US-10-372-876-275	Sequence 275, App
555	89.5	8.1	1063	15	US-10-161-493-66	Sequence 66, Appl
556	89	8.1	799	14	US-10-174-677-26	Sequence 26, Appl
557	89	8.1	799	16	US-10-678-160A-3	Sequence 3, Appli
558	88.5	8.0	1063	15	US-10-161-493-64	Sequence 64, Appl
559	88	8.0	365	9	US-09-870-759-73	Sequence 73, Appl
560	88	8.0	365	10	US-09-751-708A-73	Sequence 73, Appl
561	88	8.0	365	16	US-10-428-817A-69	Sequence 69, Appl
562	88	8.0	365	17	US-10-937-758A-50	Sequence 50, Appl
563	86.5	7.8	887	16	US-10-425-115-327399	Sequence 327399,
564	86	7.8	364	18	US-10-024-607-8	Sequence 8, Appli
565	85.5	7.8	545	14	US-10-243-243A-4	Sequence 4, Appli
566	85.5	7.8	583	14	US-10-142-515-4	Sequence 4, Appli
567	85.5	7.8	959	10	US-09-894-159-33	Sequence 33, Appl
568	85.5	7.8	959	10	US-09-894-159-95	Sequence 95, Appl
569	85.5	7.8	1148	9	US-09-884-441-458	Sequence 458, App
570	85.5	7.8	1148	9	US-09-884-441-479	Sequence 479, App
571	85.5	7.8	1148	10	US-09-907-969-458	Sequence 458, App
572	85.5	7.8	1148	10	US-09-907-969-479	Sequence 479, App
573	85.5	7.8	1148	10	US-09-827-271-458	Sequence 458, App
574	85.5	7.8	1148	14	US-10-097-340-216	Sequence 216, App
575	85.5	7.8	1148	14	US-10-198-053-458	Sequence 458, App
576	85.5	7.8	1148	14	US-10-198-053-479	Sequence 479, App
577	85.5	7.8	1148	15	US-10-257-021-56	Sequence 56, Appl
578	85.5	7.8	1148	15	US-10-383-368-2	Sequence 2, Appli
579	85.5	7.8	1148	16	US-10-734-564-131	Sequence 131, App
580	85.5	7.8	1148	17	US-10-860-790-458	Sequence 458, App
581	85.5	7.8	1148	17	US-10-860-790-479	Sequence 479, App
582	85.5	7.8	1148	17	US-10-936-626-129	Sequence 129, App
583	85.5	7.8	1148	17	US-10-938-061-129	Sequence 129, App
584	85.5	7.8	1156	9	US-09-884-441-459	Sequence 459, App
585	85.5	7.8	1156	10	US-09-907-969-459	Sequence 459, App
586	85.5	7.8	1156	10	US-09-827-271-459	Sequence 459, App
587	85.5	7.8	1156	14	US-10-198-053-459	Sequence 459, App
588	85.5	7.8	1156	17	US-10-860-790-459	Sequence 459, App
589	85.5	7.8	1889	14	US-10-142-515-5	Sequence 5, Appli
590	85	7.7	1337	15	US-10-366-547-44	Sequence 44, Appl
591	84.5	7.7	339	14	US-10-291-634-3	Sequence 3, Appli
592	84.5	7.7	1188	15	US-10-291-265-338	Sequence 338, App
593	84.5	7.7	1188	15	US-10-291-265-810	Sequence 810, App
594	83.5	7.6	1337	14	US-10-390-501-2	Sequence 2, Appli
595	83.5	7.6	1337	15	US-10-366-547-42	Sequence 42, Appl
596	83.5	7.6	1337	16	US-10-723-606-2	Sequence 2, Appli
597	82.5	7.5	809	17	US-10-687-035-2	Sequence 2, Appli
598	82	7.4	1120	15	US-10-262-839-6	Sequence 6, Appli
599	82	7.4	1189	10	US-09-984-130-35	Sequence 35, Appl

600	82	7.4	1189	10	US-09-836-353A-35	Sequence 35, Appl
601	82	7.4	1189	15	US-10-262-839-4	Sequence 4, Appli
602	82	7.4	1189	16	US-10-723-860-2788	Sequence 2788, Ap
603	82	7.4	1216	15	US-10-366-547-49	Sequence 49, Appl
604	81.5	7.4	302	14	US-10-032-214-268	Sequence 268, App
605	81.5	7.4	302	18	US-10-479-901-268	Sequence 268, App
606	81.5	7.4	1048	10	US-09-920-267C-9	Sequence 9, Appli
607	81.5	7.4	1048	15	US-10-211-462-189	Sequence 189, App
608	81.5	7.4	1048	16	US-10-720-323-9	Sequence 9, Appli
609	81.5	7.4	1048	16	US-10-769-565-9	Sequence 9, Appli
610	81.5	7.4	1048	16	US-10-484-568-75	Sequence 75, Appl
611	81.5	7.4	1048	17	US-10-482-029-20	Sequence 20, Appl
612	81	7.4	1135	11	US-09-972-211-108	Sequence 108, App
613	81	7.4	1135	15	US-10-096-625-108	Sequence 108, App
614	81	7.4	1179	11	US-09-972-211-109	Sequence 109, App
615	81	7.4	1179	15	US-10-096-625-109	Sequence 109, App
616	80.5	7.3	284	10	US-09-965-738-300	Sequence 300, App
617	80.5	7.3	430	16	US-10-437-963-198596	Sequence 198596,
618	80.5	7.3	438	9	US-09-884-441-483	Sequence 483, App
619	80.5	7.3	438	10	US-09-907-969-483	Sequence 483, App
620	80.5	7.3	438	14	US-10-198-053-483	Sequence 483, App
621	80.5	7.3	438	15	US-10-333-900-19	Sequence 19, Appl
622	80.5	7.3	438	17	US-10-860-790-483	Sequence 483, App
623	80.5	7.3	439	10	US-09-965-738-148	Sequence 148, App
624	80.5	7.3	526	15	US-10-333-900-30	Sequence 30, Appl
625	80.5	7.3	1148	10	US-09-932-419-2	Sequence 2, Appli
626	80.5	7.3	1148	10	US-09-965-738-48	Sequence 48, Appl
627	80.5	7.3	2248	10	US-09-965-738-50	Sequence 50, Appl
628	80.5	7.3	11721	10	US-09-965-738-162	Sequence 162, App
629	80.5	7.3	22152	16	US-10-715-066-5	Sequence 5, Appli
630	79.5	7.2	340	15	US-10-051-874-78	Sequence 78, Appl
631	79.5	7.2	355	15	US-10-369-493-345	Sequence 345, App
632	79.5	7.2	502	14	US-10-156-761-11794	Sequence 11794, A
633	79.5	7.2	1890	14	US-10-097-340-217	Sequence 217, App
634	79.5	7.2	1890	15	US-10-245-871-314	Sequence 314, App
635	79.5	7.2	1890	15	US-10-253-286-314	Sequence 314, App
636	79.5	7.2	2234	15	US-10-612-090-20	Sequence 20, Appl
637	79	7.2	2029	15	US-10-087-684-38	Sequence 38, Appl
638	79	7.2	2029	15	US-10-218-779-38	Sequence 38, Appl
639	79	7.2	2037	15	US-10-087-684-39	Sequence 39, Appl
640	79	7.2	2037	15	US-10-218-779-39	Sequence 39, Appl
641	78.5	7.1	233	9	US-09-884-441-488	Sequence 488, App
642	78.5	7.1	233	10	US-09-907-969-488	Sequence 488, App
643	78.5	7.1	233	14	US-10-198-053-488	Sequence 488, App
644	78.5	7.1	233	17	US-10-860-790-488	Sequence 488, App
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646	78.5	7.1	318	10	US-09-907-969-594	Sequence 594, App
647	78.5	7.1	318	14	US-10-198-053-594	Sequence 594, App
648	78.5	7.1	318	17	US-10-860-790-594	Sequence 594, App
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651	78.5	7.1	438	10	US-09-827-271-390	Sequence 390, App
652	78.5	7.1	438	14	US-10-198-053-390	Sequence 390, App
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654	78.5	7.1	696	10	US-09-866-050A-501	Sequence 501, App
655	78.5	7.1	833	9	US-09-884-441-389	Sequence 389, App
656	78.5	7.1	833	10	US-09-907-969-389	Sequence 389, App
657	78.5	7.1	833	10	US-09-827-271-389	Sequence 389, App
658	78.5	7.1	833	14	US-10-198-053-389	Sequence 389, App
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661	78.5	7.1	914	9	US-09-910-689-206	Sequence 206, App
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663	78.5	7.1	914	9	US-09-884-441-478	Sequence 478, App
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666	78.5	7.1	914	10	US-09-827-271-312	Sequence 312, App
667	78.5	7.1	914	13	US-10-010-742-206	Sequence 206, App
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671	78.5	7.1	914	16	US-10-717-296-206	Sequence 206, App
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675	78.5	7.1	3451	10	US-09-907-969-595	Sequence 595, App
676	78.5	7.1	3451	14	US-10-198-053-595	Sequence 595, App
677	78.5	7.1	3451	17	US-10-860-790-595	Sequence 595, App
678	78	7.1	300	14	US-10-032-214-196	Sequence 196, App
679	78	7.1	300	18	US-10-479-901-196	Sequence 196, App
680	78	7.1	343	9	US-09-985-694A-9	Sequence 9, Appli
681	78	7.1	343	10	US-09-929-752-9	Sequence 9, Appli
682	78	7.1	343	13	US-10-176-079-9	Sequence 9, Appli
683	78	7.1	343	14	US-10-184-426-9	Sequence 9, Appli
684	78	7.1	343	14	US-10-305-555-14	Sequence 14, Appl
685	78	7.1	354	17	US-10-485-555-58	Sequence 58, Appl
686	78	7.1	555	14	US-10-288-252-9	Sequence 9, Appli
687	78	7.1	555	16	US-10-398-038-9	Sequence 9, Appli
688	78	7.1	555	17	US-10-976-440-9	Sequence 9, Appli
689	78	7.1	887	14	US-10-132-350-18	Sequence 18, Appl
690	78	7.1	887	14	US-10-132-350-20	Sequence 20, Appl
691	78	7.1	926	15	US-10-425-114-69756	Sequence 69756, A
692	77.5	7.0	232	17	US-10-495-148-33	Sequence 33, Appl
693	77.5	7.0	330	16	US-10-437-963-120185	Sequence 120185,
694	77	7.0	661	16	US-10-437-963-183011	Sequence 183011,
695	76.5	6.9	303	14	US-10-032-214-59	Sequence 59, Appl
696	76.5	6.9	303	18	US-10-479-901-59	Sequence 59, Appl
697	76.5	6.9	314	14	US-10-032-585-7686	Sequence 7686, Ap
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699	76.5	6.9	549	10	US-09-972-268-4	Sequence 4, Appli
700	76.5	6.9	549	10	US-09-972-268-6	Sequence 6, Appli
701	76.5	6.9	549	14	US-10-161-572-45	Sequence 45, Appl
702	76.5	6.9	696	15	US-10-424-599-195355	Sequence 195355,
703	76.5	6.9	794	15	US-10-072-012-484	Sequence 484, App
704	76	6.9	199	14	US-10-021-660-82	Sequence 82, Appl
705	76	6.9	230	16	US-10-408-765A-356	Sequence 356, App
706	76	6.9	820	16	US-10-437-963-131873	Sequence 131873,
707	76	6.9	906	16	US-10-437-963-131866	Sequence 131866,
708	75.5	6.9	127	15	US-10-264-237-1908	Sequence 1908, Ap
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712	75.5	6.9	255	15	US-10-417-312-6	Sequence 6, Appli
713	75.5	6.9	264	15	US-10-417-312-7	Sequence 7, Appli
714	75.5	6.9	264	15	US-10-447-839A-105	Sequence 105, App
715	75.5	6.9	273	15	US-10-417-312-4	Sequence 4, Appli
716	75.5	6.9	282	15	US-10-417-312-5	Sequence 5, Appli
717	75.5	6.9	299	14	US-10-032-214-49	Sequence 49, Appl
718	75.5	6.9	299	14	US-10-032-214-281	Sequence 281, App
719	75.5	6.9	299	18	US-10-479-901-49	Sequence 49, Appl
720	75.5	6.9	299	18	US-10-479-901-281	Sequence 281, App
721	75.5	6.9	301	14	US-10-032-214-192	Sequence 192, App
722	75.5	6.9	301	18	US-10-479-901-192	Sequence 192, App
723	75.5	6.9	302	14	US-10-032-214-62	Sequence 62, Appl
724	75.5	6.9	302	14	US-10-032-214-180	Sequence 180, App
725	75.5	6.9	302	14	US-10-032-214-195	Sequence 195, App
726	75.5	6.9	302	14	US-10-032-214-203	Sequence 203, App
727	75.5	6.9	302	14	US-10-032-214-213	Sequence 213, App
728	75.5	6.9	302	14	US-10-032-214-219	Sequence 219, App
729	75.5	6.9	302	18	US-10-479-901-62	Sequence 62, Appl
730	75.5	6.9	302	18	US-10-479-901-180	Sequence 180, App
731	75.5	6.9	302	18	US-10-479-901-195	Sequence 195, App
732	75.5	6.9	302	18	US-10-479-901-203	Sequence 203, App
733	75.5	6.9	302	18	US-10-479-901-213	Sequence 213, App
734	75.5	6.9	302	18	US-10-479-901-219	Sequence 219, App
735	75.5	6.9	303	14	US-10-032-214-204	Sequence 204, App
736	75.5	6.9	303	14	US-10-032-214-211	Sequence 211, App
737	75.5	6.9	303	18	US-10-479-901-204	Sequence 204, App
738	75.5	6.9	303	18	US-10-479-901-211	Sequence 211, App
739	75.5	6.9	312	15	US-10-296-734-824	Sequence 824, App
740	75.5	6.9	321	9	US-09-925-301-861	Sequence 861, App
741	75.5	6.9	475	15	US-10-417-312-1	Sequence 1, Appli
742	75.5	6.9	475	17	US-10-696-639-59	Sequence 59, Appl
743	75.5	6.9	475	20	US-11-055-119-67	Sequence 67, Appl
744	75.5	6.9	495	20	US-11-055-119-2	Sequence 2, Appli
745	75.5	6.9	515	14	US-10-097-340-212	Sequence 212, App

746	75.5	6.9	515	14	US-10-171-311-156	Sequence 156, App
747	75.5	6.9	515	15	US-10-612-090-19	Sequence 19, Appl
748	75.5	6.9	549	15	US-10-282-122A-42803	Sequence 42803, A
749	75.5	6.9	1255	10	US-09-996-069-10	Sequence 10, Appl
750	75.5	6.9	1255	14	US-10-171-311-158	Sequence 158, App
751	75.5	6.9	1255	14	US-10-177-293-311	Sequence 311, App
752	75.5	6.9	1255	16	US-10-734-564-120	Sequence 120, App
753	75.5	6.9	1255	17	US-10-473-484-2	Sequence 2, Appli
754	75.5	6.9	1713	14	US-10-270-333-177	Sequence 177, App
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758	75	6.8	1428	11	US-09-964-956-34	Sequence 34, Appl
759	74.5	6.8	204	16	US-10-477-527-23	Sequence 23, Appl
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762	74.5	6.8	307	14	US-10-017-161-1786	Sequence 1786, Ap
763	74.5	6.8	307	15	US-10-292-798-1442	Sequence 1442, Ap
764	74.5	6.8	307	15	US-10-343-650A-680	Sequence 680, App
765	74.5	6.8	307	16	US-10-724-208-18	Sequence 18, Appl
766	74.5	6.8	307	16	US-10-770-127-189	Sequence 189, App
767	74.5	6.8	307	16	US-10-724-209-18	Sequence 18, Appl
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773	73.5	6.7	299	18	US-10-479-901-50	Sequence 50, Appl
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775	73.5	6.7	303	14	US-10-032-214-200	Sequence 200, App
776	73.5	6.7	303	14	US-10-032-214-201	Sequence 201, App
777	73.5	6.7	303	18	US-10-479-901-188	Sequence 188, App
778	73.5	6.7	303	18	US-10-479-901-200	Sequence 200, App
779	73.5	6.7	303	18	US-10-479-901-201	Sequence 201, App
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782	73.5	6.7	498	15	US-10-369-493-9019	Sequence 9019, Ap
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789	73	6.6	14	14	US-10-319-763-28	Sequence 28, Appl
790	73	6.6	14	17	US-10-926-683-6	Sequence 6, Appli
791	73	6.6	14	17	US-10-930-331-28	Sequence 28, Appl
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794	73	6.6	205	14	US-10-050-704-98	Sequence 98, Appl
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798	73	6.6	221	14	US-10-102-806-603	Sequence 603, App
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807	73	6.6	1148	20	US-11-021-951-147	Sequence 147, App
808	73	6.6	1177	17	US-10-461-862-146	Sequence 146, App
809	73	6.6	1179	17	US-10-461-862-148	Sequence 148, App
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814	73	6.6	1181	16	US-10-473-127-280	Sequence 280, App
815	73	6.6	1181	16	US-10-473-127-282	Sequence 282, App
816	73	6.6	1181	16	US-10-473-127-283	Sequence 283, App
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818	73	6.6	1181	18	US-10-764-425-139	Sequence 139, App
819	72.5	6.6	231	15	US-10-369-493-5603	Sequence 5603, Ap
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822	72.5	6.6	302	18	US-10-479-901-272	Sequence 272, App
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832	72.5	6.6	303	18	US-10-479-901-193	Sequence 193, App
833	72.5	6.6	303	18	US-10-479-901-197	Sequence 197, App
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875	71.5	6.5	303	14	US-10-032-214-189	Sequence 189, App
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879	71.5	6.5	303	14	US-10-032-214-208	Sequence 208, App
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889	71.5	6.5	303	18	US-10-479-901-60	Sequence 60, Appl
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898	71.5	6.5	303	18	US-10-479-901-202	Sequence 202, App
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916	71.5	6.5	796	17	US-10-941-442-4	Sequence 4, Appli
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986	71	6.4	560	16	US-10-775-972-225	Sequence 225, App
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1117	71	6.4	742	16	US-10-741-601-339	Sequence 339, App
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181	67	6.1	493	4	US-09-710-279-1832	Sequence 1832, Ap
182	67	6.1	506	2	US-08-849-480A-5	Sequence 5, Appli
183	67	6.1	593	3	US-09-134-001C-3991	Sequence 3991, Ap
184	67	6.1	840	4	US-09-715-962-2	Sequence 2, Appli
185	67	6.1	841	4	US-09-949-016-9669	Sequence 9669, Ap
186	66.5	6.0	227	1	US-08-414-625-4	Sequence 4, Appli
187	66.5	6.0	231	4	US-09-189-833B-9	Sequence 9, Appli
188	66.5	6.0	325	4	US-09-651-200-20	Sequence 20, Appl
189	66.5	6.0	364	4	US-08-914-372C-12	Sequence 12, Appl
190	66.5	6.0	395	4	US-08-635-552A-4	Sequence 4, Appli
191	66.5	6.0	419	2	US-08-270-581-2	Sequence 2, Appli
192	66.5	6.0	419	4	US-09-146-893-2	Sequence 2, Appli
193	66.5	6.0	419	4	US-08-675-499A-5	Sequence 5, Appli
194	66.5	6.0	419	4	US-08-812-008-5	Sequence 5, Appli
195	66.5	6.0	423	4	US-09-778-510-22	Sequence 22, Appl
196	66.5	6.0	440	4	US-09-866-028-61	Sequence 61, Appl
197	66.5	6.0	440	4	US-09-944-457-61	Sequence 61, Appl
198	66.5	6.0	442	4	US-09-778-510-20	Sequence 20, Appl
199	66.5	6.0	442	4	US-09-930-803-1	Sequence 1, Appli
200	66.5	6.0	444	3	US-09-119-788-2	Sequence 2, Appli
201	66.5	6.0	444	4	US-09-426-290-2	Sequence 2, Appli
202	66.5	6.0	444	4	US-09-826-509-551	Sequence 551, App
203	66.5	6.0	518	3	US-08-999-723-2	Sequence 2, Appli
204	66.5	6.0	518	3	US-09-434-427-2	Sequence 2, Appli
205	66.5	6.0	518	4	US-09-548-372D-2	Sequence 2, Appli
206	66.5	6.0	518	4	US-09-548-367D-2	Sequence 2, Appli
207	66.5	6.0	518	4	US-09-551-853D-2	Sequence 2, Appli
208	66.5	6.0	518	4	US-09-215-450-19	Sequence 19, Appl
209	66.5	6.0	518	4	US-09-416-901B-2	Sequence 2, Appli
210	66.5	6.0	518	4	US-09-548-376D-2	Sequence 2, Appli
211	66.5	6.0	518	4	US-09-886-143-2	Sequence 2, Appli
212	66.5	6.0	518	4	US-09-794-927A-2	Sequence 2, Appli
213	66.5	6.0	518	4	US-09-548-373D-2	Sequence 2, Appli
214	66.5	6.0	518	4	US-09-795-847B-2	Sequence 2, Appli
215	66.5	6.0	518	4	US-09-869-414-2	Sequence 2, Appli
216	66.5	6.0	518	4	US-09-548-366F-2	Sequence 2, Appli
217	66.5	6.0	518	4	US-09-548-368D-2	Sequence 2, Appli
218	66.5	6.0	518	4	US-09-794-925A-2	Sequence 2, Appli
219	66.5	6.0	518	4	US-09-806-194A-2	Sequence 2, Appli
220	66.5	6.0	541	4	US-09-949-016-11075	Sequence 11075, A
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222	66.5	6.0	707	3	US-09-228-986-80	Sequence 80, Appl
223	66.5	6.0	707	4	US-10-101-464A-80	Sequence 80, Appl
224	66.5	6.0	1346	3	US-09-320-878-4	Sequence 4, Appli
225	66.5	6.0	1346	4	US-09-141-908-5	Sequence 5, Appli
226	66.5	6.0	1346	4	US-09-657-440-4	Sequence 4, Appli
227	66	6.0	121	4	US-09-489-039A-13007	Sequence 13007, A
228	66	6.0	353	4	US-09-203-958A-4	Sequence 4, Appli
229	66	6.0	384	2	US-08-833-226-2	Sequence 2, Appli
230	66	6.0	453	4	US-09-248-796A-14922	Sequence 14922, A
231	66	6.0	477	4	US-09-583-110-3555	Sequence 3555, Ap
232	66	6.0	482	4	US-09-107-532A-4868	Sequence 4868, Ap
233	66	6.0	605	3	US-09-394-645-2	Sequence 2, Appli
234	66	6.0	605	3	US-09-243-560B-2	Sequence 2, Appli
235	66	6.0	718	2	US-08-560-398-12	Sequence 12, Appl
236	66	6.0	723	4	US-09-328-352-6928	Sequence 6928, Ap
237	66	6.0	778	4	US-09-328-352-7907	Sequence 7907, Ap
238	66	6.0	956	1	US-08-185-232A-2	Sequence 2, Appli
239	66	6.0	956	1	US-08-416-523-2	Sequence 2, Appli
240	66	6.0	956	3	US-08-789-478-2	Sequence 2, Appli
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242	65.5	5.9	268	4	US-09-451-527-23	Sequence 23, Appl
243	65.5	5.9	269	3	US-09-430-503-2	Sequence 2, Appli
244	65.5	5.9	269	3	US-09-430-503-4	Sequence 4, Appli
245	65.5	5.9	269	3	US-09-430-503-6	Sequence 6, Appli
246	65.5	5.9	269	3	US-09-430-503-8	Sequence 8, Appli

247	65.5	5.9	294	4	US-09-322-409-7	Sequence 7, Appli
248	65.5	5.9	294	4	US-09-451-527-7	Sequence 7, Appli
249	65.5	5.9	313	4	US-09-949-016-10974	Sequence 10974, A
250	65.5	5.9	363	4	US-08-914-372C-37	Sequence 37, Appl
251	65.5	5.9	364	1	US-08-680-726A-56	Sequence 56, Appl
252	65.5	5.9	364	3	US-09-092-409-56	Sequence 56, Appl
253	65.5	5.9	364	4	US-08-914-372C-11	Sequence 11, Appl
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257	65.5	5.9	556	4	US-09-538-092-712	Sequence 712, App
258	65.5	5.9	561	4	US-09-866-510-24	Sequence 24, Appl
259	65.5	5.9	668	4	US-09-949-016-8139	Sequence 8139, Ap
260	65.5	5.9	906	1	US-08-220-151-9	Sequence 9, Appli
261	65.5	5.9	906	1	US-08-413-118-9	Sequence 9, Appli
262	65.5	5.9	906	3	US-08-473-446-9	Sequence 9, Appli
263	65.5	5.9	1090	4	US-09-866-510-14	Sequence 14, Appl
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265	65.5	5.9	1106	1	US-08-168-917-2	Sequence 2, Appli
266	65.5	5.9	1106	1	US-08-477-329-2	Sequence 2, Appli
267	65.5	5.9	1106	2	US-08-475-458-2	Sequence 2, Appli
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270	65.5	5.9	1106	3	US-08-980-400-2	Sequence 2, Appli
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273	65.5	5.9	1106	3	US-09-583-210-2	Sequence 2, Appli
274	65.5	5.9	1106	3	US-09-583-449A-2	Sequence 2, Appli
275	65.5	5.9	1106	3	US-09-435-059-2	Sequence 2, Appli
276	65.5	5.9	1106	3	US-08-461-917-4	Sequence 4, Appli
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278	65.5	5.9	1106	4	US-08-464-436-4	Sequence 4, Appli
279	65.5	5.9	1106	4	US-09-866-510-16	Sequence 16, Appl
280	65.5	5.9	1106	4	US-09-866-510-18	Sequence 18, Appl
281	65.5	5.9	1106	4	US-09-866-510-20	Sequence 20, Appl
282	65.5	5.9	1106	4	US-09-866-510-22	Sequence 22, Appl
283	65.5	5.9	1106	5	PCT-US92-00730-2	Sequence 2, Appli
284	65.5	5.9	1106	5	PCT-US92-00862-2	Sequence 2, Appli
285	65.5	5.9	1113	4	US-09-332-522E-2	Sequence 2, Appli
286	65	5.9	138	4	US-09-134-000C-6578	Sequence 6578, Ap
287	65	5.9	146	4	US-09-582-337-12	Sequence 12, Appl
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289	65	5.9	156	4	US-09-270-767-48413	Sequence 48413, A
290	65	5.9	250	3	US-09-134-001C-4399	Sequence 4399, Ap
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292	65	5.9	448	4	US-09-252-991A-18545	Sequence 18545, A
293	65	5.9	534	4	US-09-710-279-920	Sequence 920, App
294	65	5.9	535	4	US-09-326-480A-3	Sequence 3, Appli
295	65	5.9	667	1	US-07-879-617A-8	Sequence 8, Appli
296	65	5.9	667	1	US-08-753-985-8	Sequence 8, Appli
297	65	5.9	855	1	US-08-336-343A-4	Sequence 4, Appli
298	65	5.9	887	4	US-09-949-016-11126	Sequence 11126, A
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306	64.5	5.9	234	4	US-09-915-593-2	Sequence 2, Appli
307	64.5	5.9	240	4	US-09-512-363-6	Sequence 6, Appli
308	64.5	5.9	240	4	US-09-176-200-6	Sequence 6, Appli
309	64.5	5.9	240	4	US-09-915-593-6	Sequence 6, Appli
310	64.5	5.9	270	3	US-09-085-305-20	Sequence 20, Appl
311	64.5	5.9	357	4	US-09-902-540-9903	Sequence 9903, Ap
312	64.5	5.9	381	4	US-09-540-236-3615	Sequence 3615, Ap
313	64.5	5.9	404	4	US-09-252-991A-18546	Sequence 18546, A
314	64.5	5.9	464	2	US-08-602-725-32	Sequence 32, Appl
315	64.5	5.9	464	4	US-09-949-016-6116	Sequence 6116, Ap
316	64.5	5.9	464	4	US-09-949-016-7525	Sequence 7525, Ap
317	64.5	5.9	556	4	US-09-248-796A-23187	Sequence 23187, A
318	64.5	5.9	581	4	US-09-851-985-4	Sequence 4, Appli
319	64.5	5.9	694	4	US-09-851-985-2	Sequence 2, Appli
320	64.5	5.9	906	4	US-09-417-039-11	Sequence 11, Appl
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322	64.5	5.9	913	2	US-08-474-068A-6	Sequence 6, Appli
323	64.5	5.9	913	2	US-08-472-481-5	Sequence 5, Appli
324	64.5	5.9	1346	3	US-09-105-537-37	Sequence 37, Appl
325	64.5	5.9	11877	3	US-09-105-537-6	Sequence 6, Appli
326	64	5.8	150	4	US-09-248-796A-23394	Sequence 23394, A
327	64	5.8	199	4	US-09-902-540-9868	Sequence 9868, Ap
328	64	5.8	231	4	US-09-949-016-7831	Sequence 7831, Ap
329	64	5.8	250	4	US-09-252-991A-33027	Sequence 33027, A
330	64	5.8	329	4	US-09-651-200-19	Sequence 19, Appl
331	64	5.8	330	2	US-08-332-562A-134	Sequence 134, App
332	64	5.8	352	4	US-09-252-991A-30568	Sequence 30568, A
333	64	5.8	406	4	US-09-270-767-32002	Sequence 32002, A
334	64	5.8	406	4	US-09-270-767-47219	Sequence 47219, A
335	64	5.8	449	4	US-09-640-419C-24	Sequence 24, Appl
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337	64	5.8	563	4	US-09-535-315-23	Sequence 23, Appl
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339	64	5.8	856	4	US-09-619-353-8	Sequence 8, Appli
340	64	5.8	862	4	US-09-751-687-9	Sequence 9, Appli
341	64	5.8	862	4	US-09-751-687-12	Sequence 12, Appl
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344	64	5.8	1212	3	US-09-090-535-2	Sequence 2, Appli
345	64	5.8	1212	3	US-09-090-535-3	Sequence 3, Appli
346	64	5.8	1212	3	US-09-090-535-4	Sequence 4, Appli
347	63.5	5.8	92	4	US-09-640-211A-947	Sequence 947, App
348	63.5	5.8	253	4	US-09-543-681A-8042	Sequence 8042, Ap
349	63.5	5.8	272	4	US-09-949-016-5936	Sequence 5936, Ap
350	63.5	5.8	317	4	US-09-543-681A-4789	Sequence 4789, Ap
351	63.5	5.8	361	4	US-08-914-372C-8	Sequence 8, Appli
352	63.5	5.8	361	4	US-08-914-372C-9	Sequence 9, Appli
353	63.5	5.8	382	4	US-09-248-796A-14294	Sequence 14294, A
354	63.5	5.8	395	4	US-09-550-115-8	Sequence 8, Appli
355	63.5	5.8	431	4	US-09-866-028-83	Sequence 83, Appl
356	63.5	5.8	431	4	US-09-944-457-83	Sequence 83, Appl
357	63.5	5.8	485	3	US-09-320-878-10	Sequence 10, Appl
358	63.5	5.8	485	3	US-09-105-537-10	Sequence 10, Appl
359	63.5	5.8	485	4	US-09-141-908-23	Sequence 23, Appl
360	63.5	5.8	485	4	US-09-657-440-10	Sequence 10, Appl
361	63.5	5.8	533	4	US-09-508-370A-6	Sequence 6, Appli
362	63.5	5.8	535	4	US-09-949-016-10290	Sequence 10290, A
363	63.5	5.8	674	4	US-09-949-016-7196	Sequence 7196, Ap
364	63.5	5.8	681	4	US-09-543-681A-5453	Sequence 5453, Ap
365	63.5	5.8	699	5	PCT-US94-07297-39	Sequence 39, Appl
366	63.5	5.8	821	4	US-09-438-185A-155	Sequence 155, App
367	63.5	5.8	835	4	US-09-619-353-7	Sequence 7, Appli
368	63.5	5.8	906	4	US-09-367-895-41	Sequence 41, Appl
369	63.5	5.8	921	1	US-08-396-479B-2	Sequence 2, Appli
370	63.5	5.8	921	1	US-08-818-823-2	Sequence 2, Appli
371	63.5	5.8	980	1	US-08-091-569-2	Sequence 2, Appli
372	63.5	5.8	980	1	US-08-203-676-2	Sequence 2, Appli
373	63.5	5.8	980	2	US-08-822-238-2	Sequence 2, Appli
374	63.5	5.8	1171	4	US-09-417-197-131	Sequence 131, App
375	63.5	5.8	1181	4	US-09-417-197-133	Sequence 133, App
376	63.5	5.8	1330	4	US-09-543-681A-8057	Sequence 8057, Ap
377	63.5	5.8	3782	3	US-09-105-537-4	Sequence 4, Appli
378	63	5.7	133	4	US-09-861-451A-56	Sequence 56, Appl
379	63	5.7	138	4	US-09-647-468-172	Sequence 172, App
380	63	5.7	169	4	US-09-524-101D-8	Sequence 8, Appli
381	63	5.7	182	4	US-09-328-352-4216	Sequence 4216, Ap
382	63	5.7	289	4	US-09-270-767-40192	Sequence 40192, A
383	63	5.7	289	4	US-09-270-767-55408	Sequence 55408, A
384	63	5.7	301	4	US-09-489-039A-9064	Sequence 9064, Ap
385	63	5.7	302	4	US-09-107-532A-5635	Sequence 5635, Ap
386	63	5.7	310	4	US-09-543-681A-6858	Sequence 6858, Ap
387	63	5.7	315	4	US-09-949-016-11121	Sequence 11121, A
388	63	5.7	315	4	US-09-949-016-11122	Sequence 11122, A
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390	63	5.7	362	6	5504194-2	Patent No. 5504194
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392	63	5.7	396	4	US-09-555-062B-4	Sequence 4, Appli

393	63	5.7	452	4	US-09-711-164-366	Sequence 366, App
394	63	5.7	521	4	US-09-489-039A-8118	Sequence 8118, Ap
395	63	5.7	632	4	US-09-949-016-10386	Sequence 10386, A
396	63	5.7	673	4	US-09-583-110-2860	Sequence 2860, Ap
397	63	5.7	691	4	US-09-107-433-3567	Sequence 3567, Ap
398	63	5.7	762	3	US-09-228-986-114	Sequence 114, App
399	63	5.7	762	4	US-10-101-464A-114	Sequence 114, App
400	63	5.7	934	4	US-09-902-540-14209	Sequence 14209, A
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402	63	5.7	1132	4	US-09-569-098A-87	Sequence 87, Appl
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404	62.5	5.7	115	4	US-09-540-236-2698	Sequence 2698, Ap
405	62.5	5.7	234	4	US-09-492-709A-350	Sequence 350, App
406	62.5	5.7	237	4	US-09-248-796A-14858	Sequence 14858, A
407	62.5	5.7	289	2	US-08-580-545B-4	Sequence 4, Appli
408	62.5	5.7	289	3	US-09-262-653A-4	Sequence 4, Appli
409	62.5	5.7	289	3	US-08-867-484A-2	Sequence 2, Appli
410	62.5	5.7	289	4	US-09-760-892-2	Sequence 2, Appli
411	62.5	5.7	320	3	US-09-256-000-17	Sequence 17, Appl
412	62.5	5.7	320	4	US-10-034-015A-17	Sequence 17, Appl
413	62.5	5.7	386	1	US-08-758-213-1	Sequence 1, Appli
414	62.5	5.7	386	2	US-08-692-787-48	Sequence 48, Appl
415	62.5	5.7	386	3	US-09-097-199-48	Sequence 48, Appl
416	62.5	5.7	386	4	US-09-248-796A-15279	Sequence 15279, A
417	62.5	5.7	386	4	US-09-949-016-6022	Sequence 6022, Ap
418	62.5	5.7	391	4	US-09-583-110-5170	Sequence 5170, Ap
419	62.5	5.7	392	4	US-09-107-433-3904	Sequence 3904, Ap
420	62.5	5.7	403	4	US-09-489-039A-13550	Sequence 13550, A
421	62.5	5.7	413	4	US-09-248-796A-18131	Sequence 18131, A
422	62.5	5.7	414	1	US-08-188-228-52	Sequence 52, Appl
423	62.5	5.7	414	1	US-08-332-643-46	Sequence 46, Appl
424	62.5	5.7	414	1	US-08-332-638-52	Sequence 52, Appl
425	62.5	5.7	421	4	US-09-668-262A-16	Sequence 16, Appl
426	62.5	5.7	428	4	US-09-173-300-36	Sequence 36, Appl
427	62.5	5.7	428	4	US-10-027-450-36	Sequence 36, Appl
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429	62.5	5.7	466	4	US-10-034-015A-2	Sequence 2, Appli
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433	62.5	5.7	505	3	US-09-382-256-16	Sequence 16, Appl
434	62.5	5.7	505	3	US-09-395-115-16	Sequence 16, Appl
435	62.5	5.7	505	3	US-08-123-934A-8	Sequence 8, Appli
436	62.5	5.7	505	3	US-08-436-265-16	Sequence 16, Appl
437	62.5	5.7	505	3	US-09-679-187-16	Sequence 16, Appl
438	62.5	5.7	505	4	US-09-874-628-8	Sequence 8, Appli
439	62.5	5.7	505	4	US-09-267-963D-16	Sequence 16, Appl
440	62.5	5.7	505	5	PCT-US94-10080-8	Sequence 8, Appli
441	62.5	5.7	513	4	US-09-489-039A-9245	Sequence 9245, Ap
442	62.5	5.7	515	2	US-09-146-283-2	Sequence 2, Appli
443	62.5	5.7	515	3	US-08-579-823A-2	Sequence 2, Appli
444	62.5	5.7	515	3	US-09-344-195-2	Sequence 2, Appli
445	62.5	5.7	533	3	US-09-256-000-19	Sequence 19, Appl
446	62.5	5.7	533	4	US-10-034-015A-19	Sequence 19, Appl
447	62.5	5.7	554	4	US-09-543-681A-5774	Sequence 5774, Ap
448	62.5	5.7	580	3	US-09-256-000-21	Sequence 21, Appl
449	62.5	5.7	580	4	US-10-034-015A-21	Sequence 21, Appl
450	62.5	5.7	593	2	US-08-987-466-1	Sequence 1, Appli
451	62.5	5.7	593	3	US-09-240-359-1	Sequence 1, Appli
452	62.5	5.7	613	4	US-09-949-016-11085	Sequence 11085, A
453	62.5	5.7	635	4	US-09-538-092-1	Sequence 1, Appli
454	62.5	5.7	635	4	US-10-101-464A-932	Sequence 932, App
455	62.5	5.7	645	4	US-09-345-473E-15	Sequence 15, Appl
456	62.5	5.7	645	4	US-09-345-473E-16	Sequence 16, Appl
457	62.5	5.7	649	3	US-09-188-930-305	Sequence 305, App
458	62.5	5.7	649	4	US-09-312-283C-305	Sequence 305, App
459	62.5	5.7	653	1	US-08-188-228-46	Sequence 46, Appl
460	62.5	5.7	653	1	US-08-332-638-46	Sequence 46, Appl
461	62.5	5.7	662	4	US-09-949-016-10298	Sequence 10298, A
462	62.5	5.7	672	4	US-10-162-012-30	Sequence 30, Appl
463	62.5	5.7	693	4	US-09-248-796A-16667	Sequence 16667, A
464	62.5	5.7	721	4	US-09-949-016-10436	Sequence 10436, A
465	62.5	5.7	816	4	US-09-949-016-7437	Sequence 7437, Ap
466	62.5	5.7	888	1	US-08-445-640-35	Sequence 35, Appl
467	62.5	5.7	888	3	US-08-170-558-35	Sequence 35, Appl
468	62.5	5.7	888	3	US-08-447-314-35	Sequence 35, Appl
469	62.5	5.7	888	3	US-08-445-461-35	Sequence 35, Appl
470	62.5	5.7	888	4	US-09-223-490-35	Sequence 35, Appl
471	62.5	5.7	894	1	US-08-372-892-2	Sequence 2, Appli
472	62.5	5.7	894	1	US-08-445-640-34	Sequence 34, Appl
473	62.5	5.7	894	3	US-08-170-558-34	Sequence 34, Appl
474	62.5	5.7	894	3	US-08-447-314-34	Sequence 34, Appl
475	62.5	5.7	894	3	US-08-445-461-34	Sequence 34, Appl
476	62.5	5.7	894	4	US-09-223-490-34	Sequence 34, Appl
477	62.5	5.7	907	1	US-08-349-006-2	Sequence 2, Appli
478	62.5	5.7	907	3	US-08-804-439A-19	Sequence 19, Appl
479	62.5	5.7	907	3	US-08-720-229-19	Sequence 19, Appl
480	62.5	5.7	907	4	US-09-171-699-2	Sequence 2, Appli
481	62.5	5.7	907	5	PCT-US94-04180-2	Sequence 2, Appli
482	62.5	5.7	975	4	US-09-949-016-7595	Sequence 7595, Ap
483	62.5	5.7	1132	4	US-09-248-796A-15026	Sequence 15026, A
484	62.5	5.7	1333	3	US-09-356-952-2	Sequence 2, Appli
485	62.5	5.7	1333	4	US-09-976-594-312	Sequence 312, App
486	62	5.6	136	4	US-09-647-468-155	Sequence 155, App
487	62	5.6	145	4	US-09-621-976-4037	Sequence 4037, Ap
488	62	5.6	220	3	US-08-228-208A-21	Sequence 21, Appl
489	62	5.6	223	1	US-08-505-058-5	Sequence 5, Appli
490	62	5.6	223	2	US-08-459-818-25	Sequence 25, Appl
491	62	5.6	223	2	US-08-889-666-25	Sequence 25, Appl
492	62	5.6	223	2	US-08-465-078-25	Sequence 25, Appl
493	62	5.6	223	2	US-08-725-776-25	Sequence 25, Appl
494	62	5.6	223	2	US-08-488-062-25	Sequence 25, Appl
495	62	5.6	250	4	US-09-322-409-31	Sequence 31, Appl
496	62	5.6	250	4	US-09-451-527-31	Sequence 31, Appl
497	62	5.6	273	4	US-09-910-174B-2	Sequence 2, Appli
498	62	5.6	273	4	US-09-620-461-2	Sequence 2, Appli
499	62	5.6	276	4	US-09-322-409-26	Sequence 26, Appl
500	62	5.6	276	4	US-09-451-527-26	Sequence 26, Appl
501	62	5.6	294	4	US-09-328-352-6415	Sequence 6415, Ap
502	62	5.6	307	2	US-08-332-562A-83	Sequence 83, Appl
503	62	5.6	331	4	US-09-107-433-3138	Sequence 3138, Ap
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508	62	5.6	365	4	US-09-270-767-50028	Sequence 50028, A
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510	62	5.6	393	4	US-09-949-016-6572	Sequence 6572, Ap
511	62	5.6	412	3	US-09-134-001C-4885	Sequence 4885, Ap
512	62	5.6	431	4	US-09-949-016-10578	Sequence 10578, A
513	62	5.6	462	4	US-09-949-016-8272	Sequence 8272, Ap
514	62	5.6	483	4	US-09-336-115C-20	Sequence 20, Appl
515	62	5.6	630	4	US-10-355-975A-38	Sequence 38, Appl
516	62	5.6	642	4	US-09-248-796A-14875	Sequence 14875, A
517	62	5.6	685	4	US-10-101-464A-918	Sequence 918, App
518	62	5.6	834	1	US-08-471-033-21	Sequence 21, Appl
519	62	5.6	834	2	US-08-471-044-21	Sequence 21, Appl
520	62	5.6	834	2	US-08-463-483A-21	Sequence 21, Appl
521	62	5.6	834	2	US-08-471-046A-21	Sequence 21, Appl
522	62	5.6	834	2	US-08-470-566B-21	Sequence 21, Appl
523	62	5.6	834	2	US-08-469-334-21	Sequence 21, Appl
524	62	5.6	834	3	US-09-300-529-21	Sequence 21, Appl
525	62	5.6	885	1	US-08-372-892-4	Sequence 4, Appli
526	62	5.6	885	4	US-09-919-497-52	Sequence 52, Appl
527	62	5.6	975	4	US-09-252-991A-28749	Sequence 28749, A
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531	62	5.6	1969	4	US-09-839-479-71	Sequence 71, Appl
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533	61.5	5.6	143	4	US-09-270-767-50724	Sequence 50724, A
534	61.5	5.6	176	4	US-09-540-236-3039	Sequence 3039, Ap
535	61.5	5.6	216	4	US-09-354-221-6	Sequence 6, Appli
536	61.5	5.6	216	5	PCT-US96-12129B-2	Sequence 2, Appli
537	61.5	5.6	241	3	US-08-911-423-4	Sequence 4, Appli
538	61.5	5.6	241	4	US-09-512-363-4	Sequence 4, Appli

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541	61.5	5.6	241	4	US-09-915-593-4	Sequence 4, Appli
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546	61.5	5.6	325	4	US-09-215-569B-6	Sequence 6, Appli
547	61.5	5.6	366	4	US-09-328-352-6796	Sequence 6796, Ap
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555	61.5	5.6	505	3	US-09-395-115-8	Sequence 8, Appli
556	61.5	5.6	505	3	US-08-436-265-8	Sequence 8, Appli
557	61.5	5.6	505	3	US-09-679-187-8	Sequence 8, Appli
558	61.5	5.6	505	4	US-09-267-963D-8	Sequence 8, Appli
559	61.5	5.6	505	4	US-09-949-016-10260	Sequence 10260, A
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561	61.5	5.6	505	4	US-09-949-016-10262	Sequence 10262, A
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563	61.5	5.6	631	4	US-10-355-975A-11	Sequence 11, Appl
564	61.5	5.6	793	4	US-09-107-532A-5141	Sequence 5141, Ap
565	61.5	5.6	825	4	US-09-921-667-16	Sequence 16, Appl
566	61.5	5.6	825	4	US-09-949-001-14	Sequence 14, Appl
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568	61.5	5.6	839	4	US-09-949-001-26	Sequence 26, Appl
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571	61	5.5	273	2	US-08-834-108-10	Sequence 10, Appl
572	61	5.5	303	4	US-09-252-991A-31930	Sequence 31930, A
573	61	5.5	369	4	US-08-462-509B-4	Sequence 4, Appli
574	61	5.5	369	5	PCT-US95-05616-4	Sequence 4, Appli
575	61	5.5	372	4	US-08-462-509B-6	Sequence 6, Appli
576	61	5.5	377	5	PCT-US95-05616-6	Sequence 6, Appli
577	61	5.5	389	2	US-08-846-705-2	Sequence 2, Appli
578	61	5.5	389	4	US-09-211-823C-23	Sequence 23, Appl
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580	61	5.5	402	4	US-08-462-509B-2	Sequence 2, Appli
581	61	5.5	402	5	PCT-US95-05616-2	Sequence 2, Appli
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584	61	5.5	416	2	US-08-834-108-2	Sequence 2, Appli
585	61	5.5	419	1	US-08-385-186-4	Sequence 4, Appli
586	61	5.5	419	4	US-09-328-352-6670	Sequence 6670, Ap
587	61	5.5	425	3	US-08-846-704-2	Sequence 2, Appli
588	61	5.5	425	3	US-09-479-128-2	Sequence 2, Appli
589	61	5.5	425	4	US-09-211-823C-22	Sequence 22, Appl
590	61	5.5	425	4	US-09-826-509-549	Sequence 549, App
591	61	5.5	430	4	US-09-198-452A-1038	Sequence 1038, Ap
592	61	5.5	436	4	US-09-438-185A-968	Sequence 968, App
593	61	5.5	464	1	US-08-252-995D-6	Sequence 6, Appli
594	61	5.5	464	2	US-08-834-108-6	Sequence 6, Appli
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596	61	5.5	510	1	US-08-249-112-3	Sequence 3, Appli
597	61	5.5	510	5	PCT-US95-06556-3	Sequence 3, Appli
598	61	5.5	546	4	US-09-907-794A-250	Sequence 250, App
599	61	5.5	546	4	US-09-905-125A-250	Sequence 250, App
600	61	5.5	546	4	US-09-902-775A-250	Sequence 250, App
601	61	5.5	546	4	US-09-906-700-250	Sequence 250, App
602	61	5.5	546	4	US-09-903-603A-250	Sequence 250, App
603	61	5.5	546	4	US-09-904-920A-250	Sequence 250, App
604	61	5.5	546	4	US-09-909-064-250	Sequence 250, App
605	61	5.5	546	4	US-09-905-381A-250	Sequence 250, App
606	61	5.5	546	4	US-09-906-618-250	Sequence 250, App
607	61	5.5	554	4	US-09-614-891-11	Sequence 11, Appl
608	61	5.5	597	3	US-08-844-274-12	Sequence 12, Appl
609	61	5.5	597	4	US-09-598-421-12	Sequence 12, Appl
610	61	5.5	639	4	US-09-270-767-61294	Sequence 61294, A
611	61	5.5	662	4	US-09-134-000C-5682	Sequence 5682, Ap
612	61	5.5	764	4	US-09-270-767-45772	Sequence 45772, A
613	61	5.5	780	4	US-09-785-381-11	Sequence 11, Appl
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615	61	5.5	892	4	US-09-248-796A-15642	Sequence 15642, A
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617	61	5.5	925	2	US-08-834-108-4	Sequence 4, Appli
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621	60.5	5.5	199	4	US-09-270-767-46939	Sequence 46939, A
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623	60.5	5.5	233	2	US-09-024-848-4	Sequence 4, Appli
624	60.5	5.5	233	3	US-09-348-116A-4	Sequence 4, Appli
625	60.5	5.5	236	2	US-08-070-116A-2	Sequence 2, Appli
626	60.5	5.5	236	4	US-08-557-050-2	Sequence 2, Appli
627	60.5	5.5	241	1	US-08-188-228-56	Sequence 56, Appl
628	60.5	5.5	241	1	US-08-332-643-50	Sequence 50, Appl
629	60.5	5.5	241	1	US-08-332-638-56	Sequence 56, Appl
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633	60.5	5.5	292	3	US-09-348-116A-2	Sequence 2, Appli
634	60.5	5.5	292	3	US-09-345-468-18	Sequence 18, Appl
635	60.5	5.5	292	3	US-09-414-453A-18	Sequence 18, Appl
636	60.5	5.5	301	4	US-09-270-767-33112	Sequence 33112, A
637	60.5	5.5	301	4	US-09-270-767-48329	Sequence 48329, A
638	60.5	5.5	313	3	US-09-345-468-16	Sequence 16, Appl
639	60.5	5.5	313	3	US-09-414-453A-16	Sequence 16, Appl
640	60.5	5.5	347	4	US-09-107-433-2714	Sequence 2714, Ap
641	60.5	5.5	364	4	US-08-914-372C-10	Sequence 10, Appl
642	60.5	5.5	370	4	US-09-583-110-4976	Sequence 4976, Ap
643	60.5	5.5	376	1	US-08-253-155A-33	Sequence 33, Appl
644	60.5	5.5	380	4	US-09-270-767-44518	Sequence 44518, A
645	60.5	5.5	398	4	US-09-192-012-2	Sequence 2, Appli
646	60.5	5.5	447	3	US-09-370-253-10	Sequence 10, Appl
647	60.5	5.5	449	4	US-09-583-110-3602	Sequence 3602, Ap
648	60.5	5.5	457	4	US-09-595-990A-2	Sequence 2, Appli
649	60.5	5.5	470	4	US-09-107-433-2658	Sequence 2658, Ap
650	60.5	5.5	482	4	US-09-538-092-1345	Sequence 1345, Ap
651	60.5	5.5	513	4	US-09-270-767-37275	Sequence 37275, A
652	60.5	5.5	513	4	US-09-270-767-52492	Sequence 52492, A
653	60.5	5.5	544	4	US-09-489-039A-14296	Sequence 14296, A
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656	60.5	5.5	948	4	US-09-248-796A-19297	Sequence 19297, A
657	60.5	5.5	958	4	US-09-706-594-5	Sequence 5, Appli
658	60.5	5.5	1051	4	US-09-949-016-6190	Sequence 6190, Ap
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661	60	5.4	238	4	US-09-949-016-11628	Sequence 11628, A
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663	60	5.4	274	4	US-09-915-524-19	Sequence 19, Appl
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665	60	5.4	281	4	US-10-101-464A-518	Sequence 518, App
666	60	5.4	306	4	US-09-270-767-38494	Sequence 38494, A
667	60	5.4	306	4	US-09-270-767-53711	Sequence 53711, A
668	60	5.4	325	4	US-09-198-452A-992	Sequence 992, App
669	60	5.4	331	4	US-09-438-185A-922	Sequence 922, App
670	60	5.4	336	4	US-09-248-796A-24750	Sequence 24750, A
671	60	5.4	355	2	US-08-846-762-93	Sequence 93, Appl
672	60	5.4	370	4	US-09-134-000C-5739	Sequence 5739, Ap
673	60	5.4	376	4	US-09-902-540-13960	Sequence 13960, A
674	60	5.4	377	4	US-09-328-352-7154	Sequence 7154, Ap
675	60	5.4	411	4	US-09-252-991A-31301	Sequence 31301, A
676	60	5.4	414	4	US-09-710-279-806	Sequence 806, App
677	60	5.4	415	4	US-09-543-681A-7191	Sequence 7191, Ap
678	60	5.4	423	3	US-09-134-001C-3599	Sequence 3599, Ap
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680	60	5.4	428	4	US-10-029-715-5	Sequence 5, Appli
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683	60	5.4	502	4	US-09-902-540-11457	Sequence 11457, A
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691	60	5.4	592	4	US-09-690-359-47	Sequence 47, Appl
692	60	5.4	597	3	US-08-867-611-16	Sequence 16, Appl
693	60	5.4	597	4	US-09-690-359-16	Sequence 16, Appl
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696	60	5.4	690	3	US-08-816-977-47	Sequence 47, Appl
697	60	5.4	690	4	US-09-334-477-47	Sequence 47, Appl
698	60	5.4	694	3	US-08-816-977-49	Sequence 49, Appl
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707	60	5.4	1375	3	US-09-210-361-4	Sequence 4, Appli
708	60	5.4	1375	4	US-09-740-274-4	Sequence 4, Appli
709	60	5.4	2319	1	US-08-212-133A-8	Sequence 8, Appli
710	60	5.4	2319	1	US-08-474-503-6	Sequence 6, Appli
711	60	5.4	2319	2	US-08-670-707A-6	Sequence 6, Appli
712	60	5.4	2319	3	US-09-037-601-6	Sequence 6, Appli
713	60	5.4	2319	3	US-09-315-179-6	Sequence 6, Appli
714	60	5.4	2319	4	US-09-523-656-28	Sequence 28, Appl
715	60	5.4	2319	5	PCT-US94-13200-6	Sequence 6, Appli
716	59.5	5.4	209	3	US-09-109-100-8	Sequence 8, Appli
717	59.5	5.4	209	3	US-09-109-100-9	Sequence 9, Appli
718	59.5	5.4	209	3	US-09-109-100-11	Sequence 11, Appl
719	59.5	5.4	209	3	US-09-109-100-12	Sequence 12, Appl
720	59.5	5.4	209	3	US-09-109-100-13	Sequence 13, Appl
721	59.5	5.4	209	3	US-09-109-100-17	Sequence 17, Appl
722	59.5	5.4	209	3	US-09-109-100-18	Sequence 18, Appl
723	59.5	5.4	212	3	US-09-109-100-10	Sequence 10, Appl
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728	59.5	5.4	231	1	US-08-220-379B-7	Sequence 7, Appli
729	59.5	5.4	231	1	US-08-243-545-2	Sequence 2, Appli
730	59.5	5.4	231	2	US-08-993-962-2	Sequence 2, Appli
731	59.5	5.4	231	3	US-09-160-841-2	Sequence 2, Appli
732	59.5	5.4	231	4	US-08-669-692-2	Sequence 2, Appli
733	59.5	5.4	231	4	US-08-444-626-2	Sequence 2, Appli
734	59.5	5.4	231	5	PCT-US94-05365-2	Sequence 2, Appli
735	59.5	5.4	231	5	PCT-US95-03866-6	Sequence 6, Appli
736	59.5	5.4	235	1	US-08-243-545-6	Sequence 6, Appli
737	59.5	5.4	235	2	US-08-993-962-6	Sequence 6, Appli
738	59.5	5.4	235	3	US-09-160-841-6	Sequence 6, Appli
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742	59.5	5.4	235	5	PCT-US94-05365-6	Sequence 6, Appli
743	59.5	5.4	238	4	US-09-270-767-31899	Sequence 31899, A
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745	59.5	5.4	247	4	US-09-949-016-11350	Sequence 11350, A
746	59.5	5.4	263	3	US-09-134-001C-4998	Sequence 4998, Ap
747	59.5	5.4	264	4	US-09-107-532A-6300	Sequence 6300, Ap
748	59.5	5.4	269	4	US-10-000-489-78	Sequence 78, Appl
749	59.5	5.4	271	4	US-09-479-040-23	Sequence 23, Appl
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752	59.5	5.4	304	4	US-09-328-352-6202	Sequence 6202, Ap
753	59.5	5.4	315	4	US-09-949-016-7014	Sequence 7014, Ap
754	59.5	5.4	325	4	US-09-215-569B-4	Sequence 4, Appli
755	59.5	5.4	354	4	US-09-393-627B-28	Sequence 28, Appl
756	59.5	5.4	364	1	US-08-385-186-9	Sequence 9, Appli
757	59.5	5.4	368	5	PCT-US93-11703-24	Sequence 24, Appl
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760	59.5	5.4	380	2	US-09-073-674-16	Sequence 16, Appl
761	59.5	5.4	398	4	US-09-348-930A-9	Sequence 9, Appli
762	59.5	5.4	398	4	US-09-578-063-75	Sequence 75, Appl
763	59.5	5.4	414	1	US-08-614-801A-4	Sequence 4, Appli
764	59.5	5.4	415	4	US-09-540-236-2213	Sequence 2213, Ap
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766	59.5	5.4	433	4	US-09-489-039A-9762	Sequence 9762, Ap
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770	59.5	5.4	502	3	US-08-436-265-12	Sequence 12, Appl
771	59.5	5.4	502	3	US-09-679-187-12	Sequence 12, Appl
772	59.5	5.4	502	4	US-09-267-963D-12	Sequence 12, Appl
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774	59.5	5.4	717	4	US-10-101-464A-810	Sequence 810, App
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776	59.5	5.4	739	4	US-09-854-845-45	Sequence 45, Appl
777	59.5	5.4	744	4	US-09-854-845-43	Sequence 43, Appl
778	59.5	5.4	776	4	US-09-165-396-3	Sequence 3, Appli
779	59.5	5.4	802	4	US-09-889-746-4	Sequence 4, Appli
780	59.5	5.4	838	4	US-09-854-845-29	Sequence 29, Appl
781	59.5	5.4	843	4	US-09-854-845-27	Sequence 27, Appl
782	59.5	5.4	864	4	US-09-751-687-18	Sequence 18, Appl
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784	59.5	5.4	1038	4	US-09-215-569B-12	Sequence 12, Appl
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786	59.5	5.4	1282	4	US-09-543-681A-5419	Sequence 5419, Ap
787	59.5	5.4	2254	2	US-08-286-819A-28	Sequence 28, Appl
788	59.5	5.4	2254	3	US-08-980-357-28	Sequence 28, Appl
789	59.5	5.4	3174	2	US-08-477-451-3	Sequence 3, Appli
790	59	5.4	84	3	US-09-134-001C-3555	Sequence 3555, Ap
791	59	5.4	88	4	US-09-489-039A-8639	Sequence 8639, Ap
792	59	5.4	117	3	US-08-973-068-5	Sequence 5, Appli
793	59	5.4	146	2	US-08-449-287-10	Sequence 10, Appl
794	59	5.4	187	4	US-09-248-796A-16076	Sequence 16076, A
795	59	5.4	189	3	US-09-332-934-13	Sequence 13, Appl
796	59	5.4	189	4	US-09-949-016-6103	Sequence 6103, Ap
797	59	5.4	205	4	US-09-270-767-40123	Sequence 40123, A
798	59	5.4	205	4	US-09-270-767-55339	Sequence 55339, A
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802	59	5.4	247	4	US-09-107-433-2806	Sequence 2806, Ap
803	59	5.4	257	4	US-09-248-796A-20148	Sequence 20148, A
804	59	5.4	281	3	US-09-134-001C-4763	Sequence 4763, Ap
805	59	5.4	295	4	US-09-489-039A-8783	Sequence 8783, Ap
806	59	5.4	301	4	US-09-489-039A-10251	Sequence 10251, A
807	59	5.4	306	4	US-09-270-767-43575	Sequence 43575, A
808	59	5.4	311	4	US-09-270-767-32957	Sequence 32957, A
809	59	5.4	311	4	US-09-270-767-48174	Sequence 48174, A
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812	59	5.4	343	4	US-09-734-237B-37	Sequence 37, Appl
813	59	5.4	355	4	US-09-543-681A-5929	Sequence 5929, Ap
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816	59	5.4	371	4	US-09-328-352-6825	Sequence 6825, Ap
817	59	5.4	388	4	US-09-492-709A-378	Sequence 378, App
818	59	5.4	407	4	US-09-543-681A-7929	Sequence 7929, Ap
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823	59	5.4	447	1	US-07-978-892A-6	Sequence 6, Appli
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827	59	5.4	448	3	US-09-076-510-3	Sequence 3, Appli
828	59	5.4	448	4	US-09-004-349-3	Sequence 3, Appli
829	59	5.4	449	4	US-09-198-452A-575	Sequence 575, App
830	59	5.4	453	1	US-07-937-609-26	Sequence 26, Appl

831	59	5.4	453	3	US-08-029-170-26	Sequence 26, Appl
832	59	5.4	453	4	US-09-443-745-26	Sequence 26, Appl
833	59	5.4	464	4	US-09-438-185A-538	Sequence 538, App
834	59	5.4	510	4	US-09-711-164-365	Sequence 365, App
835	59	5.4	519	3	US-09-522-217-85	Sequence 85, Appl
836	59	5.4	519	4	US-09-923-246-85	Sequence 85, Appl
837	59	5.4	519	4	US-10-295-723-85	Sequence 85, Appl
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839	59	5.4	596	3	US-09-134-001C-3363	Sequence 3363, Ap
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841	59	5.4	600	4	US-10-044-543-22	Sequence 22, Appl
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845	59	5.4	764	4	US-09-949-016-9890	Sequence 9890, Ap
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847	59	5.4	783	4	US-09-165-396-2	Sequence 2, Appli
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852	59	5.4	833	2	US-08-346-126-6	Sequence 6, Appli
853	59	5.4	833	2	US-08-346-128-6	Sequence 6, Appli
854	59	5.4	833	3	US-08-532-384-2	Sequence 2, Appli
855	59	5.4	833	3	US-08-893-828-6	Sequence 6, Appli
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858	59	5.4	876	3	US-08-996-621-2	Sequence 2, Appli
859	59	5.4	915	4	US-09-107-532A-3714	Sequence 3714, Ap
860	59	5.4	1203	3	US-09-075-272-4	Sequence 4, Appli
861	59	5.4	1323	1	US-08-026-138E-4	Sequence 4, Appli
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865	59	5.4	1336	3	US-08-940-035A-58	Sequence 58, Appl
866	59	5.4	1336	3	US-08-935-105A-58	Sequence 58, Appl
867	59	5.4	1336	4	US-09-648-797-58	Sequence 58, Appl
868	59	5.4	1336	4	US-09-386-123-58	Sequence 58, Appl
869	59	5.4	1336	4	US-10-038-937-58	Sequence 58, Appl
870	59	5.4	1345	4	US-09-949-016-11209	Sequence 11209, A
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874	58.5	5.3	205	4	US-09-248-796A-16932	Sequence 16932, A
875	58.5	5.3	209	3	US-09-109-100-14	Sequence 14, Appl
876	58.5	5.3	212	3	US-09-199-637A-235	Sequence 235, App
877	58.5	5.3	218	4	US-09-270-767-44628	Sequence 44628, A
878	58.5	5.3	220	4	US-09-248-796A-20150	Sequence 20150, A
879	58.5	5.3	237	4	US-09-107-532A-3825	Sequence 3825, Ap
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881	58.5	5.3	262	3	US-09-134-001C-3932	Sequence 3932, Ap
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883	58.5	5.3	303	4	US-09-107-532A-6686	Sequence 6686, Ap
884	58.5	5.3	346	4	US-09-215-569B-8	Sequence 8, Appli
885	58.5	5.3	349	4	US-09-540-236-3199	Sequence 3199, Ap
886	58.5	5.3	349	4	US-09-919-497-76	Sequence 76, Appl
887	58.5	5.3	352	4	US-09-492-709A-293	Sequence 293, App
888	58.5	5.3	352	4	US-09-949-016-11359	Sequence 11359, A
889	58.5	5.3	365	4	US-09-899-634C-4	Sequence 4, Appli
890	58.5	5.3	367	4	US-09-543-681A-4643	Sequence 4643, Ap
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893	58.5	5.3	407	4	US-09-275-252A-14	Sequence 14, Appl
894	58.5	5.3	431	4	US-09-252-991A-27202	Sequence 27202, A
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903	58.5	5.3	734	4	US-09-248-796A-16776	Sequence 16776, A
904	58.5	5.3	760	4	US-09-328-352-7293	Sequence 7293, Ap
905	58.5	5.3	807	4	US-09-538-092-574	Sequence 574, App
906	58.5	5.3	854	4	US-09-206-551-16	Sequence 16, Appl
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908	58.5	5.3	864	3	US-09-022-255-2	Sequence 2, Appli
909	58.5	5.3	864	3	US-09-022-696-2	Sequence 2, Appli
910	58.5	5.3	864	3	US-08-978-773-2	Sequence 2, Appli
911	58.5	5.3	864	3	US-09-022-253-2	Sequence 2, Appli
912	58.5	5.3	864	3	US-09-022-260-2	Sequence 2, Appli
913	58.5	5.3	864	3	US-09-022-259-2	Sequence 2, Appli
914	58.5	5.3	864	3	US-09-022-257-2	Sequence 2, Appli
915	58.5	5.3	864	4	US-09-549-679-2	Sequence 2, Appli
916	58.5	5.3	921	4	US-09-248-796A-14950	Sequence 14950, A
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919	58.5	5.3	1041	4	US-09-270-767-47836	Sequence 47836, A
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921	58.5	5.3	1198	4	US-09-284-768A-10	Sequence 10, Appl
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925	58.5	5.3	2763	3	US-08-496-944-2	Sequence 2, Appli
926	58	5.3	142	4	US-09-513-999C-6264	Sequence 6264, Ap
927	58	5.3	166	4	US-09-270-767-32448	Sequence 32448, A
928	58	5.3	166	4	US-09-270-767-47665	Sequence 47665, A
929	58	5.3	218	4	US-09-134-000C-5450	Sequence 5450, Ap
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931	58	5.3	260	3	US-09-006-353A-8	Sequence 8, Appli
932	58	5.3	260	4	US-09-573-986-8	Sequence 8, Appli
933	58	5.3	260	4	US-09-949-016-6047	Sequence 6047, Ap
934	58	5.3	272	4	US-09-538-092-551	Sequence 551, App
935	58	5.3	277	4	US-09-248-796A-21807	Sequence 21807, A
936	58	5.3	293	4	US-09-252-991A-20791	Sequence 20791, A
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939	58	5.3	317	4	US-09-252-991A-17668	Sequence 17668, A
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941	58	5.3	350	4	US-09-107-532A-7070	Sequence 7070, Ap
942	58	5.3	350	4	US-09-826-509-467	Sequence 467, App
943	58	5.3	359	3	US-09-134-001C-5618	Sequence 5618, Ap
944	58	5.3	369	3	US-09-177-249-4	Sequence 4, Appli
945	58	5.3	369	4	US-09-812-283-4	Sequence 4, Appli
946	58	5.3	388	4	US-09-248-796A-18287	Sequence 18287, A
947	58	5.3	398	4	US-09-778-510-4	Sequence 4, Appli
948	58	5.3	408	2	US-08-742-440A-6	Sequence 6, Appli
949	58	5.3	435	4	US-09-489-039A-7287	Sequence 7287, Ap
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953	58	5.3	449	3	US-09-076-510-1	Sequence 1, Appli
954	58	5.3	449	4	US-09-004-349-1	Sequence 1, Appli
955	58	5.3	451	1	US-08-570-157-2	Sequence 2, Appli
956	58	5.3	451	3	US-09-076-510-2	Sequence 2, Appli
957	58	5.3	451	4	US-09-004-349-2	Sequence 2, Appli
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959	58	5.3	452	3	US-08-029-170-16	Sequence 16, Appl
960	58	5.3	452	4	US-09-443-745-16	Sequence 16, Appl
961	58	5.3	453	1	US-07-937-609-27	Sequence 27, Appl
962	58	5.3	453	1	US-07-978-892A-5	Sequence 5, Appli
963	58	5.3	453	1	US-08-570-157-4	Sequence 4, Appli
964	58	5.3	453	3	US-08-029-170-27	Sequence 27, Appl
965	58	5.3	453	3	US-09-076-510-4	Sequence 4, Appli
966	58	5.3	453	4	US-09-004-349-4	Sequence 4, Appli
967	58	5.3	453	4	US-09-443-745-27	Sequence 27, Appl
968	58	5.3	480	4	US-09-540-236-3551	Sequence 3551, Ap
969	58	5.3	561	2	US-08-532-795-2	Sequence 2, Appli
970	58	5.3	569	2	US-08-532-795-23	Sequence 23, Appl
971	58	5.3	569	2	US-08-532-795-29	Sequence 29, Appl
972	58	5.3	570	2	US-08-532-795-25	Sequence 25, Appl
973	58	5.3	571	2	US-08-532-795-19	Sequence 19, Appl
974	58	5.3	571	2	US-08-532-795-21	Sequence 21, Appl
975	58	5.3	571	4	US-09-538-092-737	Sequence 737, App
976	58	5.3	574	2	US-08-532-795-27	Sequence 27, Appl

977	58	5.3	604	4	US-09-345-473E-17	Sequence 17, Appl
978	58	5.3	614	1	US-08-262-338A-4	Sequence 4, Appli
979	58	5.3	614	1	US-08-460-114A-4	Sequence 4, Appli
980	58	5.3	614	3	US-09-347-878-38	Sequence 38, Appl
981	58	5.3	614	4	US-09-133-966A-4	GENERAL INFORMA
982	58	5.3	623	3	US-09-232-200-89	Sequence 89, Appl
983	58	5.3	623	3	US-09-232-200-98	Sequence 98, Appl
984	58	5.3	623	3	US-09-232-197-89	Sequence 89, Appl
985	58	5.3	623	3	US-09-232-197-98	Sequence 98, Appl
986	58	5.3	623	3	US-09-232-201-89	Sequence 89, Appl
987	58	5.3	623	3	US-09-232-201-98	Sequence 98, Appl
988	58	5.3	623	4	US-09-232-195-89	Sequence 89, Appl
989	58	5.3	623	4	US-09-232-195-98	Sequence 98, Appl
990	58	5.3	772	4	US-09-134-000C-6491	Sequence 6491, Ap
991	58	5.3	802	3	US-09-147-236-4	Sequence 4, Appli
992	58	5.3	802	4	US-09-522-474-4	Sequence 4, Appli
993	58	5.3	806	3	US-08-549-515-5	Sequence 5, Appli
994	58	5.3	806	3	US-08-549-515-11	Sequence 11, Appl
995	58	5.3	837	3	US-09-012-710-12	Sequence 12, Appl
996	58	5.3	837	3	US-09-556-273-12	Sequence 12, Appl
997	58	5.3	873	4	US-09-248-796A-20365	Sequence 20365, A
998	58	5.3	895	1	US-08-123-161A-8	Sequence 8, Appli
999	58	5.3	895	1	US-08-483-278-8	Sequence 8, Appli
1000	58	5.3	895	4	US-09-949-016-6490	Sequence 6490, Ap
1001	58	5.3	920	4	US-09-949-016-7178	Sequence 7178, Ap
1002	58	5.3	935	4	US-09-134-000C-6493	Sequence 6493, Ap
1003	58	5.3	1084	1	US-08-717-515-6	Sequence 6, Appli
1004	58	5.3	1276	1	US-08-717-515-8	Sequence 8, Appli
1005	58	5.3	1575	4	US-09-917-254-83	Sequence 83, Appl
1006	58	5.3	1575	4	US-09-949-016-6743	Sequence 6743, Ap
1007	57.5	5.2	68	3	US-09-134-001C-5490	Sequence 5490, Ap
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1013	57.5	5.2	155	4	US-09-107-532A-5264	Sequence 5264, Ap
1014	57.5	5.2	157	3	US-09-134-001C-3371	Sequence 3371, Ap
1015	57.5	5.2	170	4	US-09-270-767-37641	Sequence 37641, A
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1017	57.5	5.2	188	4	US-09-489-039A-13189	Sequence 13189, A
1018	57.5	5.2	200	4	US-09-710-279-2126	Sequence 2126, Ap
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1026	57.5	5.2	269	4	US-09-949-016-6121	Sequence 6121, Ap
1027	57.5	5.2	276	4	US-09-949-016-7261	Sequence 7261, Ap
1028	57.5	5.2	297	4	US-09-270-767-42154	Sequence 42154, A
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1030	57.5	5.2	311	3	US-08-911-423-8	Sequence 8, Appli
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1033	57.5	5.2	319	3	US-09-375-419-12	Sequence 12, Appl
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1039	57.5	5.2	346	3	US-09-134-001C-5196	Sequence 5196, Ap
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1042	57.5	5.2	377	4	US-09-949-016-10068	Sequence 10068, A
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1044	57.5	5.2	390	4	US-09-812-216-2	Sequence 2, Appli
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1073	57.5	5.2	402	3	US-09-170-936-21	Sequence 21, Appl
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1077	57.5	5.2	402	4	US-08-643-321-20	Sequence 20, Appl
1078	57.5	5.2	402	4	US-09-148-925C-29	Sequence 29, Appl
1079	57.5	5.2	402	4	US-08-957-425-29	Sequence 29, Appl
1080	57.5	5.2	402	4	US-08-260-675-21	Sequence 21, Appl
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1088	57.5	5.2	402	5	PCT-US93-08885-21	Sequence 21, Appl
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1092	57.5	5.2	447	4	US-10-082-272-2	Sequence 2, Appli
1093	57.5	5.2	452	4	US-09-949-016-9081	Sequence 9081, Ap
1094	57.5	5.2	455	4	US-09-198-452A-372	Sequence 372, App
1095	57.5	5.2	455	4	US-09-198-452A-1028	Sequence 1028, Ap
1096	57.5	5.2	455	4	US-09-438-185A-357	Sequence 357, App
1097	57.5	5.2	455	4	US-09-438-185A-958	Sequence 958, App
1098	57.5	5.2	484	4	US-09-538-092-101	Sequence 101, App
1099	57.5	5.2	490	3	US-09-126-420A-16	Sequence 16, Appl
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1104	57.5	5.2	627	3	US-08-467-574-6	Sequence 6, Appli
1105	57.5	5.2	627	3	US-09-217-345-6	Sequence 6, Appli
1106	57.5	5.2	627	4	US-09-892-985-6	Sequence 6, Appli
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1109	57.5	5.2	753	4	US-09-949-016-11393	Sequence 11393, A
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1113	57.5	5.2	837	2	US-08-474-068A-7	Sequence 7, Appli
1114	57.5	5.2	837	2	US-08-472-481-6	Sequence 6, Appli
1115	57.5	5.2	878	1	US-08-237-919-2	Sequence 2, Appli
1116	57.5	5.2	878	3	US-08-732-429-2	Sequence 2, Appli
1117	57.5	5.2	878	4	US-09-798-267-2	Sequence 2, Appli
1118	57.5	5.2	878	4	US-09-798-267-3	Sequence 3, Appli
1119	57.5	5.2	878	5	PCT-US95-05518-2	Sequence 2, Appli
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1122	57.5	5.2	932	4	US-08-468-024B-4	Sequence 4, Appli

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1126	57.5	5.2	932	4	US-09-788-657-18	Sequence 18, Appl
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1128	57.5	5.2	932	4	US-09-707-468C-9	Sequence 9, Appli
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1133	57.5	5.2	1228	4	US-09-889-572-2	Sequence 2, Appli
1134	57.5	5.2	1228	4	US-09-117-447-2	Sequence 2, Appli
1135	57.5	5.2	1249	4	US-09-538-092-1031	Sequence 1031, Ap
1136	57.5	5.2	1249	4	US-09-949-016-6338	Sequence 6338, Ap
1137	57.5	5.2	1254	4	US-09-949-016-9737	Sequence 9737, Ap
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1139	57.5	5.2	1336	2	US-08-290-731C-6	Sequence 6, Appli
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1143	57.5	5.2	1835	3	US-09-404-650-5	Sequence 5, Appli
1144	57.5	5.2	1835	4	US-09-935-541-5	Sequence 5, Appli
1145	57	5.2	76	4	US-09-134-000C-3740	Sequence 3740, Ap
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1147	57	5.2	114	3	US-09-134-001C-5025	Sequence 5025, Ap
1148	57	5.2	148	4	US-09-134-000C-5009	Sequence 5009, Ap
1149	57	5.2	163	4	US-09-270-767-61961	Sequence 61961, A
1150	57	5.2	174	4	US-09-710-279-1520	Sequence 1520, Ap
1151	57	5.2	208	4	US-09-328-352-5111	Sequence 5111, Ap
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1153	57	5.2	216	3	US-09-134-001C-3870	Sequence 3870, Ap
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1155	57	5.2	225	1	US-08-505-058-3	Sequence 3, Appli
1156	57	5.2	225	2	US-08-459-818-23	Sequence 23, Appl
1157	57	5.2	225	2	US-08-889-666-23	Sequence 23, Appl
1158	57	5.2	225	2	US-08-465-078-23	Sequence 23, Appl
1159	57	5.2	225	2	US-08-725-776-23	Sequence 23, Appl
1160	57	5.2	225	2	US-08-488-062-23	Sequence 23, Appl
1161	57	5.2	226	4	US-09-134-000C-3747	Sequence 3747, Ap
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1163	57	5.2	228	4	US-09-512-363-7	Sequence 7, Appli
1164	57	5.2	228	4	US-09-176-200-7	Sequence 7, Appli
1165	57	5.2	228	4	US-09-915-593-7	Sequence 7, Appli
1166	57	5.2	229	4	US-08-916-442-2	Sequence 2, Appli
1167	57	5.2	229	4	US-09-731-924A-2	Sequence 2, Appli
1168	57	5.2	229	4	US-09-317-641-2	Sequence 2, Appli
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1170	57	5.2	260	4	US-09-252-991A-20351	Sequence 20351, A
1171	57	5.2	263	4	US-09-248-796A-14400	Sequence 14400, A
1172	57	5.2	265	4	US-09-328-352-8071	Sequence 8071, Ap
1173	57	5.2	279	3	US-08-339-214-24	Sequence 24, Appl
1174	57	5.2	279	3	US-08-339-214-32	Sequence 32, Appl
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1182	57	5.2	352	4	US-09-949-016-6781	Sequence 6781, Ap
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1184	57	5.2	374	4	US-09-949-016-7689	Sequence 7689, Ap
1185	57	5.2	377	3	US-09-410-464-8	Sequence 8, Appli
1186	57	5.2	379	4	US-09-107-433-4510	Sequence 4510, Ap
1187	57	5.2	382	4	US-09-328-352-4335	Sequence 4335, Ap
1188	57	5.2	397	3	US-08-948-997-5	Sequence 5, Appli
1189	57	5.2	397	3	US-09-348-817A-5	Sequence 5, Appli
1190	57	5.2	397	4	US-09-722-292-5	Sequence 5, Appli
1191	57	5.2	414	4	US-09-755-665-14	Sequence 14, Appl
1192	57	5.2	414	4	US-09-755-665-55	Sequence 55, Appl
1193	57	5.2	414	4	US-09-755-665-56	Sequence 56, Appl
1194	57	5.2	415	4	US-09-461-325-134	Sequence 134, App
1195	57	5.2	415	4	US-10-012-542-134	Sequence 134, App
1196	57	5.2	415	4	US-10-115-123-134	Sequence 134, App
1197	57	5.2	427	4	US-09-270-767-45426	Sequence 45426, A
1198	57	5.2	432	4	US-09-917-254-80	Sequence 80, Appl
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1203	57	5.2	457	3	US-08-471-961-3	Sequence 3, Appli
1204	57	5.2	457	4	US-09-345-109C-3	Sequence 3, Appli
1205	57	5.2	458	3	US-08-464-258B-3	Sequence 3, Appli
1206	57	5.2	484	4	US-09-328-352-4849	Sequence 4849, Ap
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1212	57	5.2	669	2	US-08-459-009-8	Sequence 8, Appli
1213	57	5.2	669	3	US-08-459-951-8	Sequence 8, Appli
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1218	57	5.2	774	2	US-08-486-273A-42	Sequence 42, Appl
1219	57	5.2	774	3	US-08-480-474-42	Sequence 42, Appl
1220	57	5.2	774	3	US-08-940-086A-42	Sequence 42, Appl
1221	57	5.2	774	3	US-08-940-035A-42	Sequence 42, Appl
1222	57	5.2	774	3	US-08-935-105A-42	Sequence 42, Appl
1223	57	5.2	774	4	US-09-648-797-42	Sequence 42, Appl
1224	57	5.2	774	4	US-09-386-123-42	Sequence 42, Appl
1225	57	5.2	774	4	US-10-038-937-42	Sequence 42, Appl
1226	57	5.2	787	1	US-08-453-695A-110	Sequence 110, App
1227	57	5.2	787	1	US-08-268-161A-110	Sequence 110, App
1228	57	5.2	787	2	US-08-453-702A-110	Sequence 110, App
1229	57	5.2	787	3	US-09-099-639-110	Sequence 110, App
1230	57	5.2	787	5	PCT-US95-08071-110	Sequence 110, App
1231	57	5.2	952	4	US-09-270-767-41680	Sequence 41680, A
1232	57	5.2	1021	4	US-10-101-464A-954	Sequence 954, App
1233	57	5.2	1075	1	US-07-623-033-2	Sequence 2, Appli
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1235	57	5.2	1149	4	US-09-949-016-7682	Sequence 7682, Ap
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1237	57	5.2	1214	2	US-08-231-193A-54	Sequence 54, Appl
1238	57	5.2	1214	2	US-08-486-273A-54	Sequence 54, Appl
1239	57	5.2	1214	3	US-08-480-474-54	Sequence 54, Appl
1240	57	5.2	1214	3	US-08-940-086A-54	Sequence 54, Appl
1241	57	5.2	1214	3	US-08-940-035A-54	Sequence 54, Appl
1242	57	5.2	1214	3	US-08-935-105A-54	Sequence 54, Appl
1243	57	5.2	1214	4	US-09-648-797-54	Sequence 54, Appl
1244	57	5.2	1214	4	US-09-386-123-54	Sequence 54, Appl
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1247	57	5.2	1219	2	US-08-486-273A-50	Sequence 50, Appl
1248	57	5.2	1219	3	US-08-480-474-50	Sequence 50, Appl
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1253	57	5.2	1219	4	US-09-386-123-50	Sequence 50, Appl
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1257	57	5.2	1231	3	US-08-480-474-48	Sequence 48, Appl
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1262	57	5.2	1231	4	US-09-386-123-48	Sequence 48, Appl
1263	57	5.2	1231	4	US-10-038-937-48	Sequence 48, Appl
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1267	57	5.2	1236	3	US-08-940-086A-6	Sequence 6, Appli
1268	57	5.2	1236	3	US-08-940-035A-6	Sequence 6, Appli

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1272	57	5.2	1236	4	US-10-038-937-6	Sequence 6, Appli
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1282	57	5.2	1239	4	US-10-038-937-52	Sequence 52, Appl
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1315	56.5	5.1	170	4	US-09-438-185A-176	Sequence 176, App
1316	56.5	5.1	177	4	US-09-270-767-43412	Sequence 43412, A
1317	56.5	5.1	194	4	US-09-640-211A-802	Sequence 802, App
1318	56.5	5.1	252	4	US-09-252-991A-17553	Sequence 17553, A
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1325	56.5	5.1	327	3	US-09-184-826-3	Sequence 3, Appli
1326	56.5	5.1	327	4	US-09-832-464-3	Sequence 3, Appli
1327	56.5	5.1	338	3	US-09-134-001C-5155	Sequence 5155, Ap
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1330	56.5	5.1	366	4	US-09-489-039A-7522	Sequence 7522, Ap
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1334	56.5	5.1	373	3	US-09-412-184-26	Sequence 26, Appl
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1337	56.5	5.1	393	2	US-08-793-958-15	Sequence 15, Appl
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1344	56.5	5.1	398	4	US-09-579-845-4	Sequence 4, Appli
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1346	56.5	5.1	398	4	US-09-921-667-8	Sequence 8, Appli
1347	56.5	5.1	398	5	PCT-US91-03478-2	Sequence 2, Appli
1348	56.5	5.1	402	4	US-09-543-681A-6953	Sequence 6953, Ap
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1350	56.5	5.1	413	4	US-09-543-681A-5108	Sequence 5108, Ap
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1352	56.5	5.1	445	4	US-09-328-352-4631	Sequence 4631, Ap
1353	56.5	5.1	461	4	US-09-949-016-8508	Sequence 8508, Ap
1354	56.5	5.1	481	4	US-09-902-540-13111	Sequence 13111, A
1355	56.5	5.1	482	4	US-09-328-352-6084	Sequence 6084, Ap
1356	56.5	5.1	488	4	US-09-248-796A-18644	Sequence 18644, A
1357	56.5	5.1	490	4	US-09-248-796A-23937	Sequence 23937, A
1358	56.5	5.1	500	3	US-09-292-768-4	Sequence 4, Appli
1359	56.5	5.1	500	3	US-09-292-768-68	Sequence 68, Appl
1360	56.5	5.1	500	3	US-09-292-768-70	Sequence 70, Appl
1361	56.5	5.1	507	4	US-09-328-352-7742	Sequence 7742, Ap
1362	56.5	5.1	522	3	US-09-142-732-2	Sequence 2, Appli
1363	56.5	5.1	522	4	US-08-945-826-2	Sequence 2, Appli
1364	56.5	5.1	522	4	US-09-197-503-2	Sequence 2, Appli
1365	56.5	5.1	522	4	US-09-489-039A-10999	Sequence 10999, A
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1367	56.5	5.1	529	1	US-07-779-890-2	Sequence 2, Appli
1368	56.5	5.1	529	5	PCT-US93-05640-2	Sequence 2, Appli
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1374	56.5	5.1	640	4	US-09-907-794A-292	Sequence 292, App
1375	56.5	5.1	640	4	US-09-905-125A-292	Sequence 292, App
1376	56.5	5.1	640	4	US-09-902-775A-292	Sequence 292, App
1377	56.5	5.1	640	4	US-09-906-700-292	Sequence 292, App
1378	56.5	5.1	640	4	US-09-903-603A-292	Sequence 292, App
1379	56.5	5.1	640	4	US-09-904-920A-292	Sequence 292, App
1380	56.5	5.1	640	4	US-09-909-064-292	Sequence 292, App
1381	56.5	5.1	640	4	US-09-905-381A-292	Sequence 292, App
1382	56.5	5.1	640	4	US-09-906-618-292	Sequence 292, App
1383	56.5	5.1	649	1	US-08-477-476-2	Sequence 2, Appli
1384	56.5	5.1	649	2	US-08-993-210-2	Sequence 2, Appli
1385	56.5	5.1	649	5	PCT-US96-07354-2	Sequence 2, Appli
1386	56.5	5.1	650	3	US-09-310-463-2	Sequence 2, Appli
1387	56.5	5.1	650	4	US-08-842-248A-2	Sequence 2, Appli
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1389	56.5	5.1	651	4	US-09-546-049-22	Sequence 22, Appl
1390	56.5	5.1	664	4	US-09-823-038A-48	Sequence 48, Appl
1391	56.5	5.1	664	4	US-09-902-540-12181	Sequence 12181, A
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1393	56.5	5.1	729	4	US-09-543-681A-8257	Sequence 8257, Ap
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1395	56.5	5.1	732	4	US-09-270-767-53882	Sequence 53882, A
1396	56.5	5.1	761	4	US-09-949-016-6880	Sequence 6880, Ap
1397	56.5	5.1	771	4	US-09-902-540-12980	Sequence 12980, A
1398	56.5	5.1	783	4	US-09-949-016-7187	Sequence 7187, Ap
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1402	56.5	5.1	916	1	US-08-332-638-48	Sequence 48, Appl
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1407	56.5	5.1	1051	4	US-09-911-882-14	Sequence 14, Appl
1408	56.5	5.1	1051	4	US-09-911-888-14	Sequence 14, Appl
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1411	56.5	5.1	1090	4	US-09-245-039-3	Sequence 3, Appli
1412	56.5	5.1	1090	5	PCT-US95-11808-3	Sequence 3, Appli
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1414	56.5	5.1	1972	4	US-09-839-479-21	Sequence 21, Appl

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1418	56	5.1	125	4	US-09-248-796A-16431	Sequence 16431, A
1419	56	5.1	137	4	US-09-513-999C-7963	Sequence 7963, Ap
1420	56	5.1	138	4	US-09-647-468-167	Sequence 167, App
1421	56	5.1	140	4	US-10-101-464A-530	Sequence 530, App
1422	56	5.1	146	4	US-09-582-337-10	Sequence 10, Appl
1423	56	5.1	155	4	US-09-270-767-60154	Sequence 60154, A
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1425	56	5.1	168	4	US-09-949-016-8494	Sequence 8494, Ap
1426	56	5.1	169	4	US-09-543-681A-4307	Sequence 4307, Ap
1427	56	5.1	222	4	US-09-902-540-11510	Sequence 11510, A
1428	56	5.1	229	3	US-09-134-001C-4241	Sequence 4241, Ap
1429	56	5.1	243	4	US-09-248-796A-16807	Sequence 16807, A
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1431	56	5.1	256	4	US-09-489-039A-13853	Sequence 13853, A
1432	56	5.1	257	4	US-09-205-258-421	Sequence 421, App
1433	56	5.1	261	4	US-09-540-236-2122	Sequence 2122, Ap
1434	56	5.1	272	4	US-09-489-039A-10410	Sequence 10410, A
1435	56	5.1	277	4	US-09-270-767-46151	Sequence 46151, A
1436	56	5.1	286	4	US-09-949-016-6318	Sequence 6318, Ap
1437	56	5.1	300	4	US-09-270-767-44700	Sequence 44700, A
1438	56	5.1	302	4	US-09-489-039A-12820	Sequence 12820, A
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1441	56	5.1	325	1	US-08-469-203A-9	Sequence 9, Appli
1442	56	5.1	325	1	US-08-469-203A-9	Sequence 9, Appli
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1448	56	5.1	355	3	US-09-143-438-6	Sequence 6, Appli
1449	56	5.1	356	4	US-09-270-767-46120	Sequence 46120, A
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1457	56	5.1	398	4	US-09-907-794A-84	Sequence 84, Appl
1458	56	5.1	398	4	US-09-905-125A-84	Sequence 84, Appl
1459	56	5.1	398	4	US-09-902-775A-84	Sequence 84, Appl
1460	56	5.1	398	4	US-09-906-700-84	Sequence 84, Appl
1461	56	5.1	398	4	US-09-903-603A-84	Sequence 84, Appl
1462	56	5.1	398	4	US-09-904-920A-84	Sequence 84, Appl
1463	56	5.1	398	4	US-09-909-064-84	Sequence 84, Appl
1464	56	5.1	398	4	US-09-905-381A-84	Sequence 84, Appl
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1468	56	5.1	404	3	US-09-134-001C-4261	Sequence 4261, Ap
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1471	56	5.1	409	1	US-08-440-542-21	Sequence 21, Appl
1472	56	5.1	409	1	US-08-440-542-24	Sequence 24, Appl
1473	56	5.1	409	1	US-08-231-368-21	Sequence 21, Appl
1474	56	5.1	409	1	US-08-231-368-24	Sequence 24, Appl
1475	56	5.1	409	1	US-08-440-210-21	Sequence 21, Appl
1476	56	5.1	409	1	US-08-440-210-24	Sequence 24, Appl
1477	56	5.1	409	3	US-09-046-604-21	Sequence 21, Appl
1478	56	5.1	409	3	US-09-046-604-24	Sequence 24, Appl
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1480	56	5.1	432	4	US-09-778-510-2	Sequence 2, Appli
1481	56	5.1	461	4	US-09-248-796A-23597	Sequence 23597, A
1482	56	5.1	467	4	US-09-248-796A-16430	Sequence 16430, A
1483	56	5.1	469	4	US-09-328-352-4250	Sequence 4250, Ap
1484	56	5.1	471	4	US-09-543-681A-7497	Sequence 7497, Ap
1485	56	5.1	491	4	US-09-248-796A-22333	Sequence 22333, A
1486	56	5.1	499	4	US-09-134-000C-6069	Sequence 6069, Ap
1487	56	5.1	508	4	US-09-328-352-6467	Sequence 6467, Ap
1488	56	5.1	519	4	US-09-107-532A-6778	Sequence 6778, Ap
1489	56	5.1	524	4	US-09-252-991A-18092	Sequence 18092, A
1490	56	5.1	558	4	US-09-949-016-8851	Sequence 8851, Ap
1491	56	5.1	594	3	US-08-867-611-48	Sequence 48, Appl
1492	56	5.1	594	4	US-09-690-359-48	Sequence 48, Appl
1493	56	5.1	599	3	US-08-867-611-18	Sequence 18, Appl
1494	56	5.1	599	4	US-09-690-359-18	Sequence 18, Appl
1495	56	5.1	599	5	PCT-US92-06965A-23	Sequence 23, Appl
1496	56	5.1	623	4	US-09-949-016-11206	Sequence 11206, A
1497	56	5.1	646	4	US-09-949-016-6728	Sequence 6728, Ap
1498	56	5.1	646	4	US-09-653-961-2	Sequence 2, Appli
1499	56	5.1	646	4	US-09-653-961-4	Sequence 4, Appli
1500	56	5.1	651	4	US-09-949-016-8426	Sequence 8426, Ap

ALIGNMENTS

```
RESULT 1
US-08-989-299-2
; Sequence 2, Application US/08989299
; Patent No. 6194556
;  GENERAL INFORMATION:
;    APPLICANT:  Acton, Susan L.
;    APPLICANT:  Robinson, Keith E.
;    TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG
;    TITLE OF INVENTION:  AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-2170
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/989,299
;      FILING DATE:  11-DEC-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold E., Beth
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  MIA-025.01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  805 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-989-299-2

  Query Match             34.1%;  Score 376;  DB 3;  Length 805;
  Best Local Similarity   47.9%;  Pred. No. 2.5e-34;
  Matches   79;  Conservative   32;  Mismatches   48;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::|||||||  |: || |||:: ||::||    || |:        |
Db        612 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 671

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |   :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTL 731

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPS 177
                ||  | | ||:|:|||:  :|:| | :|| :||  |::|||  |
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Db        732 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARS 776


RESULT 2
US-10-158-847-142
; Sequence 142, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-158-847-142

  Query Match             34.1%;  Score 376;  DB 4;  Length 805;
  Best Local Similarity   47.9%;  Pred. No. 2.5e-34;
  Matches   79;  Conservative   32;  Mismatches   48;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::|||||||| |: || |||:: ||::||    || |:        |
Db        612 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 671

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |   :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTL 731

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPS 177
              ||  | | ||:|:|||:  :|:| | :|| :||  |::|||  |
Db        732 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARS 776


RESULT 3
US-09-407-427-2
; Sequence 2, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
;  APPLICANT:  Acton, Susan L.
;  APPLICANT:  Robison, Keith E.
;  TITLE OF INVENTION:  ANGIOTENSIN CONVERTING ENZYME HOMOLOG  AND THERAPEUTIC
;  TITLE OF INVENTION:  AND DIAGNOSTIC USES THEREFOR
;  FILE REFERENCE:  MNI-132CP2
;  CURRENT APPLICATION NUMBER: US/09/407,427
;  CURRENT FILING DATE:  1999-09-29
;  PRIOR APPLICATION NUMBER:  09/163,648
;  PRIOR FILING DATE:  1998-09-30
;  PRIOR APPLICATION NUMBER:  08/989,299
;  PRIOR FILING DATE:  1997-12-11
;  NUMBER OF SEQ ID NOS:  14
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-407-427-2

  Query Match             34.1%;  Score 376;  DB 4;  Length 805;
  Best Local Similarity   47.9%;  Pred. No. 2.5e-34;
  Matches   79;  Conservative   32;  Mismatches   48;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::|||||||| |: || |||:: ||::||    || |:        |
Db        612 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 671

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |   :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTL 731

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPS 177
              ||  | | ||:|:|||:  :|:| | :|| :||  |::|||  |
Db        732 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARS 776


RESULT 4
US-09-949-016-11284
; Sequence 11284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11284
;   LENGTH: 819
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11284

  Query Match             34.1%;  Score 376;  DB 4;  Length 819;
  Best Local Similarity   47.9%;  Pred. No. 2.5e-34;
  Matches   79;  Conservative   32;  Mismatches   48;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::|||||||| |: || |||:: ||::||    || |:        |
Db        626 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 685

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |   :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        686 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTL 745

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPS 177
              ||  | | ||:|:|||:  :|:| | :|| :||  |::|||  |
Db        746 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARS 790


RESULT 5
US-10-158-847-138
; Sequence 138, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
;   LENGTH: 711
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (219)..(219)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
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;   NAME/KEY: MISC_FEATURE
;   LOCATION: (240)..(240)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (499)..(499)
;   OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-138

  Query Match             32.6%;  Score 359;  DB 4;  Length 711;
  Best Local Similarity   47.2%;  Pred. No. 1.9e-32;
  Matches   75;  Conservative   32;  Mismatches   46;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::|||||||  |: || |||:: ||::||    || |:        |
Db        551 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 610

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |   :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        611 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDDSLEFLGIQPTL 670

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRR 171
                ||  | | ||:|:|||:  :|:| | :|| :||  |::
Db        671 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKK 709


RESULT 6
US-10-158-847-140
; Sequence 140, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
;  APPLICANT: Tom Parry et al.
;  TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
;  FILE REFERENCE: PF557
;  CURRENT APPLICATION NUMBER: US/10/158,847
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: 60/295,004
;  PRIOR FILING DATE: 2001-06-04
;  NUMBER OF SEQ ID NOS: 158
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
;   LENGTH: 681
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (219)..(219)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (240)..(240)
;   OTHER INFORMATION: Xaa equals any amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (499)..(499)
;   OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-140

  Query Match             26.2%;  Score 289;  DB 4;  Length 681;
  Best Local Similarity   48.1%;  Pred. No. 2.2e-24;
  Matches   63;  Conservative   23;  Mismatches   39;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::|||||||  |: || |||:: ||::||    || |:        |
Db        551 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 610

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |   :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        611 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDDSLEFLGIQPTL 670

Qy        133 APPMDPSVPIW 143
                ||  | | ||
Db        671 GPPNQPPVSIW 681
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```
RESULT 7
US-08-188-228-42
; Sequence 42, Application US/08188228
; Patent No. 5597725
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  CADHERIN MATERIALS AND METHODS
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/188,228
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/049,460
;      FILING DATE:  19 APR 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,643
;      FILING DATE:  17 APR 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5597725and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31340
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  799 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-188-228-42

  Query Match              8.2%;  Score 90;  DB 1;  Length 799;
  Best Local Similarity   21.4%;  Pred. No. 0.28;
  Matches   52;  Conservative   34;  Mismatches   91;  Indels   66;  Gaps   11;

Qy         13 HAELCQPGAENAFKVRLSIRTALGDKAYAWDT---------NEEYLFKAMVAFSMRKVPN 63
              | :| :    ||   :::: | |  :   |           |   : :  ||  :  | |
Db        432 HTDLERQFNINADDGKITLATPLDRELSVWHNISIIATEIRNHSQISRVPVAIKVLDV-N 490

Qy         64 REATEIS---HVLLC------NVTQRVSFWFVVTDPSKNH-----TLPAVEVQSAIRMNK 109
                | | :      ||       | | ||      ||   |      || :      : |
Db        491 DNAPEFASEYEAFLCENGKPGQVIQTVSA-MDKDDPKNGHFFLYSLLPEMVNNPNFTIKK 549

Qy        110 NRINNAFFL------NDQTLEFLKIPSTLA----PPMDPSVPIWIIIFG---------- 148
              |  |:   |      | |  |   :|  ::    ||:  :  : | : |
Db        550 NEDNSLSILAKHNGFNRQKQEVYLLPIVISDSGNPPLSSTSTLTIRVCGCSNDGVVQSCN 609

Qy        149 ----------------VIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENMIT 191
                             :: |||:: : :::   :  || || ||  : | ||  ||:|
Db        610 VEAYVLPIGLSMGALIAILACIILLLVIVVLF--VTLRRHKN-EPLIIKDDEDVRENIIR 666

Qy        192 IEN 194
                ::
Db        667 YDD 669
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RESULT 8
US-08-332-638-42
; Sequence 42, Application US/08332638
; Patent No. 5646250
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  CADHERIN MATERIALS AND METHODS
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,638
;      FILING DATE:  01-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,643
;      FILING DATE:  17 APR 1992
;      APPLICATION NUMBER:  US/08/049,460
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5646250and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31340
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  799 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-332-638-42

  Query Match             8.2%;  Score 90;  DB 1;  Length 799;
  Best Local Similarity   21.4%;  Pred. No. 0.28;
  Matches   52;  Conservative   34;  Mismatches   91;  Indels   66;  Gaps   11;

Qy          13 HAELCQPGAENAFKVRLSIRTALGDKAYAWDT---------NEEYLFKAMVAFSMRKVPN 63
               | :| :    ||   :::: | |  :   |             |   : :  ||  :  | |
Db         432 HTDLERQFNINADDGKITLATPLDRELSVWHNISIIATEIRNHSQISRVPVAIKVLDV-N 490

Qy          64 REATEIS---HVLLC------NVTQRVSFWFVVTDPSKNH-----TLPAVEVQSAIRMNK 109
                 | | :      ||       | | ||      ||   |       || :       : |
Db         491 DNAPEFASEYEAFLCENGKPGQVIQTVSA-MDKDDPKNGHFFLYSLLPEMVNNPNFTIKK 549

Qy         110 NRINNAFFL------NDQTLEFLKIPSTLA----PPMDPSVPIWIIIFG---------- 148
               |  |:   |       | | |   :|  ::    ||:  :  : | : |
Db         550 NEDNSLSILAKHNGFNRQKQEVYLLPIVISDSGNPPLSSTSTLTIRVCGCSNDGVVQSCN 609

Qy         149 ----------------VIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENMIT 191
                             :: |||:: : :::   :  || || ||  : | ||  ||:|
Db         610 VEAYVLPIGLSMGALIAILACIILLLVIVVLF--VTLRRHKN-EPLIIKDDEDVRENIIR 666

Qy         192 IEN 194
                ::
Db         667 YDD 669


RESULT 9
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US-08-188-228-54
; Sequence 54, Application US/08188228
; Patent No. 5597725
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  CADHERIN MATERIALS AND METHODS
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/188,228
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/049,460
;      FILING DATE:  19 APR 1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,643
;      FILING DATE:  17 APR 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5597725and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31340
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  54:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  793 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-188-228-54

  Query Match             8.1%;  Score 89.5;  DB 1;  Length 793;
  Best Local Similarity   20.6%;  Pred. No. 0.32;
  Matches   50;  Conservative   35;  Mismatches   93;  Indels   65;  Gaps   10;

Qy          13 HAELCQPGAENAFKVRLSIRTALGDKAYAWDT---------NEEYLFKAMVAFSMRKVPN 63
               | :| :    ||   :::: | |  :   |             |   : :  ||  :  | |
Db         425 HTDLERQFNINADDGKITLATPLDRELSVWHNITIIATEIRNHSQISRVPVAIKVLDV-N 483

Qy          64 REATEIS---HVLLC------NVTQRVSFWFVVTDPSKNH-----TLPAVEVQSAIRMNK 109
                 | | :      ||       | | ||      ||   |       || :       : |
Db         484 DNAPEFASEYEAFLCENGKPGQVIQTVSA-MDKDDPKNGHYFLYSLLPEMVNNPNFTIKK 542

Qy         110 NRINNAFFL------NDQTLEFLKIPSTLA----PPMDPSVPIWIIIFG---------- 148
               |  |:   |       | | |   :|  ::    ||:  :  : | : |
Db         543 NEDNSLSILAKHNGFNRQKQEVYLLPIIISDSGNPPLSSTSTLTIRVCGCSNDGVVQSCN 602

Qy         149 ----------------VIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENMIT 191
                             :: |||:: : :::   :  || :  ||  : | ||  ||:|
Db         603 VEAYVLPIGLSMGALIAILACIILLLVIVVLF--VTLRRHQKNEPLIIKDDEDVRENIIR 660

Qy         192 IEN 194
                ::
Db         661 YDD 663


RESULT 10
US-08-332-643-48
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; Sequence 48, Application US/08332643
; Patent No. 5639634
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  CADHERIN MATERIALS AND METHODS
;    NUMBER OF SEQUENCES:  56
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,643
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/872,643
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5639634and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/30795
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  48:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  793 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-332-643-48

  Query Match             8.1%;  Score 89.5;  DB 1;  Length 793;
  Best Local Similarity   20.6%;  Pred. No. 0.32;
  Matches   50;  Conservative   35;  Mismatches   93;  Indels   65;  Gaps   10;

Qy         13 HAELCQPGAENAFKVRLSIRTALGDKAYAWDT---------NEEYLFKAMVAFSMRKVPN 63
              | :| :    ||   :::: | |  :   |           |   : :  ||  :  | |
Db        425 HTDLERQFNINADDGKITLATPLDRELSVWHNITIIATEIRNHSQISRVPVAIKVLDV-N 483

Qy         64 REATEIS---HVLLC------NVTQRVSFWFVVTDPSKNH-----TLPAVEVQSAIRMNK 109
              | | :      ||        | | ||      ||   |       || :       : |
Db        484 DNAPEFASEYEAFLCENGKPGQVIQTVSA-MDKDDPKNGHYFLYSLLPEMVNNPNFTIKK 542

Qy        110 NRINNAFFL------NDQTLEFLKIPSTLA----PPMDPSVPIWIIIFG---------- 148
              |  |:   |      | |  |   :|  ::    ||:  :  : | : |
Db        543 NEDNSLSILAKHNGFNRQKQEVYLLPIIISDSGNPPLSSTSTLTIRVCGCSNDGVVQSCN 602

Qy        149 ----------------VIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENMIT 191
                             :: |||:: : :::   :  || :  ||  : | ||  ||:|
Db        603 VEAYVLPIGLSMGALIAILACIILLLVIVVLF--VTLRRHQKNEPLIIKDDEDVRENIIR 660

Qy        192 IEN 194
              ::
Db        661 YDD 663


RESULT 11
US-08-332-638-54
; Sequence 54, Application US/08332638
; Patent No. 5646250
;  GENERAL INFORMATION:
;    APPLICANT:  Suzuki, Shintaro
;    TITLE OF INVENTION:  CADHERIN MATERIALS AND METHODS
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 S. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,638
;      FILING DATE:  01-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/872,643
;      FILING DATE:  17 APR 1992
;      APPLICATION NUMBER:  US/08/049,460
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5646250and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31340
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  54:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  793 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-332-638-54

  Query Match             8.1%;  Score 89.5;  DB 1;  Length 793;
  Best Local Similarity   20.6%;  Pred. No. 0.32;
  Matches   50;  Conservative   35;  Mismatches   93;  Indels   65;  Gaps   10;

Qy         13 HAELCQPGAENAFKVRLSIRTALGDKAYAWDT---------NEEYLFKAMVAFSMRKVPN 63
              | :| :    ||   :::: | |  :   |           |   : :  ||  :  | |
Db        425 HTDLERQFNINADDGKITLATPLDRELSVWHNITIIATEIRNHSQISRVPVAIKVLDV-N 483

Qy         64 REATEIS---HVLLC------NVTQRVSFWFVVTDPSKNH-----TLPAVEVQSAIRMNK 109
              | | :      ||        | | ||      ||   |       || :       : |
Db        484 DNAPEFASEYEAFLCENGKPGQVIQTVSA-MDKDDPKNGHYFLYSLLPEMVNNPNFTIKK 542

Qy        110 NRINNAFFL------NDQTLEFLKIPSTLA----PPMDPSVPIWIIIFG---------- 148
              |  |:   |      | |  |   :|  ::    ||:  :  : | : |
Db        543 NEDNSLSILAKHNGFNRQKQEVYLLPIIISDSGNPPLSSTSTLTIRVCGCSNDGVVQSCN 602

Qy        149 ----------------VIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENMIT 191
                             :: |||:: : :::   :  || :  ||  : | ||  ||:|
Db        603 VEAYVLPIGLSMGALIAILACIILLLVIVVLF--VTLRRHQKNEPLIIKDDEDVRENIIR 660

Qy        192 IEN 194
              ::
Db        661 YDD 663


RESULT 12
US-09-949-016-7423
; Sequence 7423, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

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;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7423
;   LENGTH: 715
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7423

  Query Match             8.1%;  Score 89;  DB 4;  Length 715;
  Best Local Similarity   21.4%;  Pred. No. 0.31;
  Matches   52;  Conservative   34;  Mismatches   91;  Indels   66;  Gaps   11;

Qy          13 HAELCQPGAENAFKVRLSIRTALGDKAYAWDT---------NEEYLFKAMVAFSMRKVPN 63
               | :| :    ||   :::: | |  :   |            |   : :  ||  :  | |
Db         348 HTDLERQFNINADDGKITLATPLDRELSVWHNITIIATEIRNHSQISRVPVAIKVLDV-N 406

Qy          64 REATEIS---HVLLC------NVTQRVSFWFVVTDPSKNH-----TLPAVEVQSAIRMNK 109
                 | | :      ||         | | ||       ||    |       || :     : |
Db         407 DNAPEFASEYEAFLCENGKPGQVIQTVSA-MDKDDPKNGHYFLYSLLPEMVNNPNFTIKK 465

Qy         110 NRINNAFFL------NDQTLEFLKIPSTLA----PPMDPSVPIWIIIFG---------- 148
               |  |:   |       | |  |   :|  ::    ||:  :  : | : |
Db         466 NEDNSLSILAKHNGFNRQKQEVYLLPIIISDSGNPPLSSTSTLTIRVCGCSNDGVVQSCN 525

Qy         149 -----------------VIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENMIT 191
                              :: |||:: : :::   :  || || ||  : | ||  ||:|
Db         526 VEAYVLPIGLSMGALIAILACIILLLVIVVLF--VTLRRHKN-EPLIIKDDEDVRENIIR 582

Qy         192 IEN 194
                ::
Db         583 YDD 585


RESULT 13
US-07-946-497-7
; Sequence 7, Application US/07946497
; Patent No. 5506119
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,497
;      FILING DATE:  19921109
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  mCD44
US-07-946-497-7

  Query Match             8.0%;  Score 88;  DB 1;  Length 363;
  Best Local Similarity   21.6%;  Pred. No. 0.15;
  Matches   24;  Conservative   23;  Mismatches   30;  Indels   34;  Gaps    3;

Qy         128 IPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRR---------------- 171
               : :|  |    | :| |:||   :  :: :|: | :   :  |||
Db         256 VTTTSGPMRRPQIPEWLII---LASLLALALILAVCIAVNSRRRCGQKKKLVINGGNGTV 312

Qy         172 KNKEPSEVDDAEDKCENMITIENGIPSD--------------PLDMKGGI 207
               ::::|||::    | : |: : |  ||:             :||| |:
Db         313 EDRKPSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSVDMKIGV 363


RESULT 14
US-08-483-322-7
; Sequence 7, Application US/08483322
; Patent No. 5760178
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,322
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/946,497
;      FILING DATE:  09-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  amino acid
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;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  mCD44
US-08-483-322-7

  Query Match             8.0%;  Score 88;  DB 1;  Length 363;
  Best Local Similarity   21.6%;  Pred. No. 0.15;
  Matches   24;  Conservative   23;  Mismatches   30;  Indels   34;  Gaps    3;

Qy        128 IPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRR---------------- 171
              : :|  |   | :| |:||   :  :: :|: | :   :  |||
Db        256 VTTTSGPMRRPQIPEWLII---LASLLALALILAVCIAVNSRRRCGQKKKLVINGGNGTV 312

Qy        172 KNKEPSEVDDAEDKCENMITIENGIPSD--------------PLDMKGGI 207
              ::::|||::    | : |: : |  ||:              :||| |:
Db        313 EDRKPSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSVDMKIGV 363


RESULT 15
US-08-478-882-7
; Sequence 7, Application US/08478882
; Patent No. 5885575
;  GENERAL INFORMATION:
;    APPLICANT:  HERRLICH, Peter
;    APPLICANT:  PONTA, Helmut
;    APPLICANT:  GUENTHERT, Ursula
;    APPLICANT:  MATZKU, Siegfried
;    APPLICANT:  WENZL, Achim
;    TITLE OF INVENTION:  VARIANT CD44 SURFACE PROTEINS, DNA
;    TITLE OF INVENTION:  SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
;    TITLE OF INVENTION:  AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,882
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,497
;      FILING DATE:  19921109
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16915/145
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  363 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  mCD44
US-08-478-882-7

  Query Match             8.0%;  Score 88;  DB 2;  Length 363;
  Best Local Similarity   21.6%;  Pred. No. 0.15;
  Matches   24;  Conservative   23;  Mismatches   30;  Indels   34;  Gaps    3;

Qy        128 IPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRR---------------- 171
              : :|  |   | :| |:||   :  :: :|: | :   :  |||
Db        256 VTTTSGPMRRPQIPEWLII---LASLLALALILAVCIAVNSRRRCGQKKKLVINGGNGTV 312

Qy        172 KNKEPSEVDDAEDKCENMITIENGIPSD--------------PLDMKGGI 207
              ::::|||::    | : |: : |  ||:              :||| |:
Db        313 EDRKPSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSVDMKIGV 363


Search completed: August 18, 2005, 17:33:46
Job time : 43 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2005, 17:31:04 ; Search time 172 Seconds
(without alignments)
631.167 Million cell updates/sec

Title: US-09-997-641-387
Perfect score: 1102
Sequence: 1 MLWLLFFLVTAIHAELCQPG.....ENGIPSDPLDMKGGILMMPS 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1102	100.0	212	2	Q6UW07	Q6uw07 homo sapien
2	1073	97.4	222	2	Q9HBJ8	Q9hbj8 homo sapien
3	935	84.8	222	2	Q6AYY2	Q6ayy2 rattus norv
4	928	84.2	222	2	Q9ESG4	Q9esg4 mus musculu
5	921	83.6	222	2	Q9ESG3	Q9esg3 rattus norv
6	488	44.3	228	2	Q6PE94	Q6pe94 xenopus lae
7	405	36.8	235	2	Q6P0S0	Q6p0s0 brachydanio
8	376	34.1	804	2	Q9UFZ6	Q9ufz6 homo sapien
9	376	34.1	805	2	Q9NRA7	Q9nra7 homo sapien
10	376	34.1	816	2	Q86WT0	Q86wt0 homo sapien
11	373	33.8	805	2	Q9BYF1	Q9byf1 homo sapien
12	361	32.8	805	2	Q8R0I0	Q8r0i0 mus musculu
13	357	32.4	265	2	Q9D836	Q9d836 mus musculu
14	357	32.4	798	2	Q99N71	Q99n71 mus musculu
15	100	9.1	1053	2	Q8IAQ8	Q8iaq8 plasmodium
16	97.5	8.8	1086	2	O18428	O18428 geodia cydo
17	96.5	8.8	543	2	Q8C0H7	Q8c0h7 mus musculu
18	96.5	8.8	1012	2	O70304	O70304 mus musculu
19	95.5	8.7	1406	2	Q9W6V5	Q9w6v5 gallus gall
20	93.5	8.5	929	2	Q9VR32	Q9vr32 drosophila
21	93.5	8.5	947	2	Q7RDK2	Q7rdk2 plasmodium
22	92.5	8.4	1153	1	NOS_LYMST	O61309 lymnaea sta
23	91.5	8.3	823	2	Q8CE84	Q8ce84 mus musculu
24	91.5	8.3	1188	1	ITAH_MOUSE	P61622 mus musculu
25	91.5	8.3	1188	2	Q7TQC3	Q7tqc3 mus musculu
26	91	8.3	623	1	SYR_SULTO	Q971x1 sulfolobus
27	90	8.2	716	2	Q8C449	Q8c449 mus musculu
28	90	8.2	754	2	Q8BRK4	Q8brk4 mus musculu
29	90	8.2	799	1	CAD8_MOUSE	P97291 mus musculu
30	90	8.2	799	1	CAD8_RAT	O54800 rattus norv
31	90	8.2	1608	2	Q7PR41	Q7pr41 anopheles g
32	89.5	8.1	161	2	Q9WUP8	Q9wup8 rattus norv
33	89.5	8.1	244	2	Q9C6E1	Q9c6e1 arabidopsis
34	89.5	8.1	1063	1	ITA8_HUMAN	P53708 homo sapien
35	89.5	8.1	1188	2	O76326	O76326 drosophila
36	89	8.1	481	2	Q6MA65	Q6ma65 parachlamyd
37	89	8.1	799	1	CAD8_HUMAN	P55286 homo sapien
38	89	8.1	1054	2	Q9U6S1	Q9u6s1 strongyloce
39	88.5	8.0	656	2	Q9QU36	Q9qu36 ttv-like mi
40	88	8.0	580	2	Q80X37	Q80x37 mus musculu
41	88	8.0	778	1	CD44_MOUSE	P15379 mus musculu
42	87	7.9	362	1	CD44_CRIGR	P20944 cricetulus
43	87	7.9	498	2	Q9D001	Q9d001 mus musculu
44	87	7.9	716	2	Q8C375	Q8c375 mus musculu
45	87	7.9	1326	2	Q8GHJ4	Q8ghj4 paenibacill
46	86.5	7.8	252	2	Q9FX00	Q9fx00 arabidopsis
47	86.5	7.8	956	2	Q9W4T9	Q9w4t9 drosophila
48	86.5	7.8	1063	2	Q8KCX0	Q8kcx0 chlorobium
49	86	7.8	364	2	O70509	O70509 rattus norv
50	86	7.8	431	1	CD44_MESAU	Q60522 m cd44 anti
51	86	7.8	503	1	CD44_RAT	P26051 rattus norv
52	86	7.8	780	2	O08779	O08779 rattus norv
53	85.5	7.8	667	2	Q9M3D7	Q9m3d7 arabidopsis
54	85.5	7.8	826	2	Q8IY15	Q8iy15 homo sapien
55	85.5	7.8	959	2	Q9N9Y9	Q9n9y9 drosophila
56	85.5	7.8	975	2	O97174	O97174 drosophila
57	85.5	7.8	1148	2	Q9H7S7	Q9h7s7 homo sapien
58	85.5	7.8	1865	2	Q9HCM3	Q9hcm3 homo sapien
59	84.5	7.7	252	2	Q9FGB3	Q9fgb3 arabidopsis
60	84.5	7.7	468	2	Q9JVK7	Q9jvk7 neisseria m
61	84.5	7.7	536	1	FLIF_BACSU	P23447 bacillus su
62	84.5	7.7	823	2	Q8WYI8	Q8wyi8 homo sapien
63	84.5	7.7	1033	2	O42598	O42598 xenopus lae
64	84.5	7.7	1112	2	O02344	O02344 caenorhabdi
65	84	7.6	261	2	Q8REU8	Q8reu8 fusobacteri
66	84	7.6	428	2	Q9M029	Q9m029 arabidopsis
67	84	7.6	677	2	Q8EQW3	Q8eqw3 oceanobacil
68	83.5	7.6	444	2	Q6DBH0	Q6dbh0 arabidopsis
69	83.5	7.6	1337	1	PTPJ_HUMAN	Q12913 homo sapien
70	83.5	7.6	4464	2	Q7RL36	Q7rl36 plasmodium
71	83	7.5	311	2	Q8PS66	Q8ps66 methanosarc
72	83	7.5	317	2	O97310	O97310 plasmodium
73	83	7.5	364	2	O98028	O98028 diceros bic
74	83	7.5	403	2	Q96ZT6	Q96zt6 sulfolobus
75	83	7.5	525	2	Q9KA32	Q9ka32 bacillus ha
76	83	7.5	1185	2	Q7PRK4	Q7prk4 anopheles g
77	82.5	7.5	307	2	Q6NW79	Q6nw79 brachydanio
78	82.5	7.5	330	2	O07474	O07474 staphylococ
79	82.5	7.5	436	2	Q9BK19	Q9bk19 caenorhabdi
80	82.5	7.5	465	2	Q18591	Q18591 caenorhabdi
81	82.5	7.5	527	2	Q837F6	Q837f6 enterococcu
82	82.5	7.5	1044	1	ITA8_CHICK	P26009 gallus gall
83	82	7.4	1122	2	Q6FXU4	Q6fxu4 candida gla
84	82	7.4	1189	1	ITAH_HUMAN	Q9ukx5 homo sapien
85	82	7.4	1216	2	Q62884	Q62884 rattus norv
86	81.5	7.4	224	2	Q8VSW8	Q8vsw8 staphylococ
87	81.5	7.4	252	2	O65701	O65701 arabidopsis
88	81.5	7.4	363	1	LEU3_PHOLL	Q7n128 photorhabdu
89	81.5	7.4	615	2	Q740R0	Q740r0 mycobacteri
90	81.5	7.4	773	2	Q8TGH3	Q8tgh3 malassezia
91	81.5	7.4	800	2	Q86LF9	Q86lf9 drosophila
92	81.5	7.4	801	2	Q86LF8	Q86lf8 drosophila
93	81.5	7.4	1048	1	ITAV_HUMAN	P06756 homo sapien
94	81	7.4	191	2	Q89V08	Q89v08 bradyrhizob
95	81	7.4	1041	2	O76378	O76378 lytechinus
96	81	7.4	1041	2	Q9UB90	Q9ub90 lytechinus
97	81	7.4	1179	1	ITA7_MOUSE	Q61738 mus musculu
98	80.5	7.3	257	2	Q8R6Q6	Q8r6q6 thermoanaer
99	80.5	7.3	316	2	Q92ML8	Q92ml8 rhizobium m
100	80.5	7.3	524	2	Q6F9P5	Q6f9p5 acinetobact
101	80.5	7.3	673	2	Q95YM0	Q95ym0 polyandroca
102	80.5	7.3	675	2	Q9FJI4	Q9fji4 arabidopsis
103	80.5	7.3	803	2	Q6FVI5	Q6fvi5 candida gla
104	80.5	7.3	857	2	Q90YJ4	Q90yj4 brachydanio

105	80.5	7.3	1034	1	ITAV_CHICK	P26008	gallus gall
106	80.5	7.3	6995	2	Q96RK2	Q96rk2	homo sapien
107	80.5	7.3	22152	2	Q8WXI7	Q8wxi7	homo sapien
108	80	7.3	234	1	VGP8_EBV	P03224	epstein-bar
109	80	7.3	234	2	Q777C5	Q777c5	human herpe
110	80	7.3	489	2	Q8UAK6	Q8uak6	agrobacteri
111	80	7.3	1696	2	Q6FXA2	Q6fxa2	candida gla
112	79.5	7.2	175	2	Q80Y67	Q80y67	mus musculu
113	79.5	7.2	275	2	Q64A68	Q64a68	uncultured
114	79.5	7.2	393	1	IL1S_CERAE	Q29612	cercopithec
115	79.5	7.2	502	2	Q82FJ2	Q82fj2	streptomyce
116	79.5	7.2	543	2	Q6XN32	Q6xn32	rhodococcus
117	79.5	7.2	616	2	Q9Y1A2	Q9y1a2	trypanosoma
118	79.5	7.2	1044	1	ITAV_MOUSE	P43406	mus musculu
119	79	7.2	181	2	Q9GQ05	Q9gq05	eriocheir s
120	79	7.2	370	2	Q7TSN7	Q7tsn7	mus musculu
121	79	7.2	398	2	Q9JIE1	Q9jie1	mus musculu
122	79	7.2	437	1	YC44_PORPU	P51363	porphyra pu
123	79	7.2	490	2	Q8K0G0	Q8k0g0	mus musculu
124	79	7.2	555	2	Q8BKU8	Q8bku8	mus musculu
125	79	7.2	611	1	RBT3_MOUSE	Q9ctn4	mus musculu
126	79	7.2	718	2	Q65DC6	Q65dc6	bacillus li
127	79	7.2	916	2	Q68WR4	Q68wr4	rickettsia
128	79	7.2	1016	2	Q91779	Q91779	xenopus lae
129	79	7.2	1033	1	ITAB_MOUSE	Q9qum0	mus musculu
130	79	7.2	1597	2	Q960M3	Q960m3	drosophila
131	79	7.2	2029	1	LAR_DROME	P16621	drosophila
132	79	7.2	2029	2	Q9VIS8	Q9vis8	drosophila
133	79	7.2	4057	2	Q8IJE7	Q8ije7	plasmodium
134	78.5	7.1	422	2	Q82WX0	Q82wx0	nitrosomona
135	78.5	7.1	548	2	Q9ZDV5	Q9zdv5	rickettsia
136	78.5	7.1	633	2	Q7SE53	Q7se53	neurospora
137	78.5	7.1	836	2	Q8IQ48	Q8iq48	drosophila
138	78.5	7.1	970	2	Q9U6L4	Q9u6l4	drosophila
139	78.5	7.1	1047	1	ITAV_BOVIN	P80746	bos taurus
140	78.5	7.1	1577	2	Q6BUX5	Q6bux5	debaryomyce
141	78	7.1	290	2	Q8AUN0	Q8aun0	paralabidoc
142	78	7.1	290	2	Q8AUZ6	Q8auz6	astatotilap
143	78	7.1	290	2	Q8AUZ8	Q8auz8	gaurochromi
144	78	7.1	343	1	MRGF_RAT	P23749	rattus norv
145	78	7.1	377	2	O34161	O34161	salmonella
146	78	7.1	377	2	Q7CQQ1	Q7cqq1	salmonella
147	78	7.1	504	2	O13102	O13102	carassius a
148	78	7.1	519	2	Q90425	Q90425	brachydanio
149	78	7.1	555	2	Q96K49	Q96k49	homo sapien
150	78	7.1	732	1	CADL_CHICK	P33145	gallus gall
151	78	7.1	1022	1	A1A1_ANGAN	Q92030	anguilla an
152	78	7.1	1171	2	O42094	O42094	gallus gall
153	78	7.1	2344	2	Q86117	Q86117	rabbit hemo
154	77.5	7.0	263	2	Q7P3V5	Q7p3v5	fusobacteri
155	77.5	7.0	307	2	Q74P63	Q74p63	bacillus ce
156	77.5	7.0	340	2	Q8GAT5	Q8gat5	primary end
157	77.5	7.0	351	1	CD44_CANFA	Q28284	canis famil
158	77.5	7.0	468	2	Q9K0K1	Q9k0k1	neisseria m
159	77.5	7.0	532	2	Q8KTZ2	Q8ktz2	primary end
160	77.5	7.0	686	2	Q9RDS3	Q9rds3	streptomyce
161	77.5	7.0	751	2	Q8ILK0	Q8ilk0	plasmodium
162	77.5	7.0	817	2	Q6ZPN1	Q6zpn1	mus musculu
163	77.5	7.0	991	2	Q7Z1L9	Q7z119	aplysia cal
164	77.5	7.0	1499	2	Q90815	Q90815	gallus gall
165	77.5	7.0	1727	2	Q68FD9	Q68fd9	mus musculu
166	77	7.0	118	2	Q83NU6	Q83nu6	tropheryma
167	77	7.0	308	2	Q66S57	Q66s57	oikopleura
168	77	7.0	322	1	GPT_SULSO	P96000	sulfolobus
169	77	7.0	357	2	Q6J5K1	Q6j5k1	tetraodon n
170	77	7.0	357	2	Q6J5K2	Q6j5k2	fugu rubrip
171	77	7.0	366	2	O27515	O27515	methanobact
172	77	7.0	388	2	Q8G583	Q8g583	bifidobacte
173	77	7.0	435	2	Q8E963	Q8e963	shewanella
174	77	7.0	459	2	Q8G3W8	Q8g3w8	bifidobacte
175	77	7.0	541	2	Q97DN5	Q97dn5	clostridium
176	77	7.0	699	2	Q6YVV8	Q6yvv8	oryza sativ
177	77	7.0	1045	2	Q91292	Q91292	pleurodeles
178	77	7.0	1263	2	Q7M8C9	Q7m8c9	wolinella s
179	76.5	6.9	203	2	Q7Z552	Q7z552	homo sapien
180	76.5	6.9	206	2	Q6QP95	Q6qp95	simian aden
181	76.5	6.9	304	2	Q9BVA9	Q9bva9	homo sapien
182	76.5	6.9	326	2	Q8I4P0	Q8i4p0	plasmodium
183	76.5	6.9	353	2	Q7T1C1	Q7t1c1	brachydanio
184	76.5	6.9	357	2	Q73KD7	Q73kd7	treponema d
185	76.5	6.9	363	1	LEU3_SALTY	P37412	salmonella
186	76.5	6.9	365	1	OPSR_XENLA	O12948	xenopus lae
187	76.5	6.9	385	2	Q8V3Q0	Q8v3q0	swinepox vi
188	76.5	6.9	475	1	MUC1_HYLLA	Q29435	hylobates l
189	76.5	6.9	549	2	Q9NQS3	Q9nqs3	homo sapien
190	76.5	6.9	568	2	Q870Y7	Q870y7	neurospora
191	76.5	6.9	632	2	Q9P4X1	Q9p4x1	s glycoprot
192	76.5	6.9	794	2	O93264	O93264	xenopus lae
193	76.5	6.9	895	2	Q89EH8	Q89eh8	bradyrhizob
194	76.5	6.9	945	2	Q6L465	Q61465	solanum dem
195	76	6.9	180	2	Q9YG47	Q9yg47	aeropyrum p
196	76	6.9	253	2	Q8UZE2	Q8uze2	cercopithec
197	76	6.9	291	2	Q86FD7	Q86fd7	schistosoma
198	76	6.9	306	2	Q98RE9	Q98re9	mycoplasma
199	76	6.9	362	2	O98029	O98029	diceros bic
200	76	6.9	369	2	Q98PW1	Q98pw1	mycoplasma
201	76	6.9	399	2	Q9ESE5	Q9ese5	mus musculu
202	76	6.9	542	2	O60113	O60113	schizosacch
203	76	6.9	614	2	O29599	O29599	archaeoglob
204	76	6.9	781	2	Q6TQD9	Q6tqd9	caenorhabdi
205	76	6.9	951	2	Q7UWT4	Q7uwt4	rhodopirell
206	76	6.9	1023	2	Q95Z93	Q95z93	leishmania
207	76	6.9	1023	2	Q8AY58	Q8ay58	fundulus he
208	76	6.9	1036	2	Q9TU44	Q9tu44	canis famil
209	76	6.9	1036	2	Q9TUN8	Q9tun8	canis famil
210	76	6.9	1337	1	YDM5_SCHPO	P87136	schizosacch
211	76	6.9	1416	2	Q7Q1N2	Q7q1n2	anopheles g
212	76	6.9	1509	2	Q7JM47	Q7jm47	caenorhabdi
213	76	6.9	1546	2	Q75DT4	Q75dt4	ashbya goss
214	76	6.9	1692	2	Q7JM48	Q7jm48	caenorhabdi
215	76	6.9	1888	2	Q7JM45	Q7jm45	caenorhabdi
216	76	6.9	1927	2	Q7JM46	Q7jm46	caenorhabdi
217	76	6.9	2048	2	Q7JM42	Q7jm42	caenorhabdi
218	76	6.9	2066	2	Q22190	Q22190	caenorhabdi
219	76	6.9	2101	2	Q7JM43	Q7jm43	caenorhabdi
220	76	6.9	2134	2	Q7JM44	Q7jm44	caenorhabdi
221	76	6.9	2344	2	Q86119	Q86119	rabbit hemo
222	75.5	6.9	125	2	Q7MBJ0	Q7mbj0	vibrio vuln
223	75.5	6.9	230	2	Q8YRJ3	Q8yrj3	anabaena sp
224	75.5	6.9	264	2	Q649N8	Q649n8	uncultured
225	75.5	6.9	282	2	Q7PYU2	Q7pyu2	anopheles g
226	75.5	6.9	335	2	Q15055	Q15055	homo sapien
227	75.5	6.9	348	2	Q7VNT3	Q7vnt3	haemophilus
228	75.5	6.9	350	2	Q7MUH5	Q7muh5	porphyromon
229	75.5	6.9	357	2	Q7YP06	Q7yp06	oncorhynchu
230	75.5	6.9	370	2	Q8IIZ9	Q8iiz9	plasmodium
231	75.5	6.9	385	2	Q6FDV1	Q6fdv1	acinetobact
232	75.5	6.9	407	2	Q9Y412	Q9y412	homo sapien
233	75.5	6.9	425	2	Q8A990	Q8a990	bacteroides
234	75.5	6.9	507	2	Q8B117	Q8b117	parana viru
235	75.5	6.9	507	2	Q8B120	Q8b120	parana viru
236	75.5	6.9	549	1	YJCE_ECOLI	P32703	escherichia
237	75.5	6.9	619	2	Q8SXH6	Q8sxh6	drosophila
238	75.5	6.9	653	2	O02329	O02329	caenorhabdi
239	75.5	6.9	1255	1	MUC1_HUMAN	P15941	h mucin 1 p
240	75.5	6.9	1335	2	Q9GP66	Q9gp66	drosophila
241	75.5	6.9	1335	2	Q9W1X5	Q9w1x5	drosophila
242	75.5	6.9	1713	2	Q7KW98	Q7kw98	drosophila
243	75	6.8	272	2	Q889A5	Q889a5	pseudomonas
244	75	6.8	290	2	Q8AUP1	Q8aup1	astatotilap
245	75	6.8	290	2	Q8AUZ7	Q8auz7	gaurochromi
246	75	6.8	321	2	Q6INF0	Q6inf0	xenopus lae
247	75	6.8	343	1	MRGF_MOUSE	Q8vcj6	mus musculu
248	75	6.8	357	1	OPSR_ORYLA	P87367	oryzias lat
249	75	6.8	538	2	O87359	O87359	staphylococ
250	75	6.8	538	2	Q7WU24	Q7wu24	staphylococ

251	75	6.8	668	2	Q7F0M5	Q7f0m5	oryza sativ
252	75	6.8	909	2	Q6TQE0	Q6tqe0	caenorhabdi
253	75	6.8	997	2	Q6GLU2	Q6glu2	xenopus lae
254	75	6.8	1007	1	GRD2_MOUSE	Q61625	mus musculu
255	75	6.8	1007	1	GRD2_RAT	Q63226	rattus norv
256	75	6.8	1037	2	Q6EIY7	Q6eiy7	brachydanio
257	75	6.8	1216	2	Q90Y55	Q90y55	brachydanio
258	75	6.8	1254	2	Q90Y56	Q90y56	brachydanio
259	75	6.8	1254	2	Q9YHU2	Q9yhu2	brachydanio
260	75	6.8	1428	1	ATRN_MOUSE	Q9wu60	mus musculu
261	74.5	6.8	204	2	Q8UY72	Q8uy72	simian aden
262	74.5	6.8	207	2	Q64YG0	Q64yg0	bacteroides
263	74.5	6.8	230	2	Q6F0V9	Q6f0v9	mesoplasma
264	74.5	6.8	257	2	Q8RAP8	Q8rap8	thermoanaer
265	74.5	6.8	259	2	Q9NAZ8	Q9naz8	aedes trise
266	74.5	6.8	307	1	TR41_HUMAN	P59536	homo sapien
267	74.5	6.8	348	1	RNFD_VIBPA	Q87mx1	vibrio para
268	74.5	6.8	379	1	MCP_CAVPO	P70105	cavia porce
269	74.5	6.8	469	2	Q9NC94	Q9nc94	trypanosoma
270	74.5	6.8	522	2	Q9YPA0	Q9ypa0	canine herp
271	74.5	6.8	549	2	Q7A924	Q7a924	escherichia
272	74.5	6.8	549	2	Q8X5U0	Q8x5u0	escherichia
273	74.5	6.8	549	2	Q8FAZ5	Q8faz5	escherichia
274	74.5	6.8	549	2	Q83IR1	Q83ir1	shigella fl
275	74.5	6.8	631	2	Q99K60	Q99k60	mus musculu
276	74.5	6.8	664	2	Q9M3D8	Q9m3d8	arabidopsis
277	74.5	6.8	719	2	Q6YX22	Q6yx22	oryza sativ
278	74.5	6.8	750	2	Q6YX21	Q6yx21	oryza sativ
279	74.5	6.8	787	2	Q7QHQ3	Q7qhq3	anopheles g
280	74.5	6.8	906	2	Q9XYP4	Q9xyp4	trypanosoma
281	74.5	6.8	2244	2	Q98QF2	Q98qf2	mycoplasma
282	74	6.7	199	2	Q6QPG7	Q6qpg7	simian aden
283	74	6.7	281	2	Q8CCJ1	Q8ccj1	mus musculu
284	74	6.7	288	2	Q6HDW4	Q6hdw4	bacillus th
285	74	6.7	290	2	Q8AUJ1	Q8auj1	labeotrophe
286	74	6.7	290	2	Q8AUJ2	Q8auj2	tyrannochro
287	74	6.7	290	2	Q8AUJ3	Q8auj3	pseudotroph
288	74	6.7	290	2	Q8AUJ4	Q8auj4	protomelas
289	74	6.7	290	2	Q8AUN2	Q8aun2	taeniolethr
290	74	6.7	290	2	Q8AUN3	Q8aun3	melanochrom
291	74	6.7	290	2	Q8AUN4	Q8aun4	aulonocara
292	74	6.7	290	2	Q8AUR0	Q8aur0	melanochrom
293	74	6.7	290	2	Q8AUR1	Q8aur1	cynotilapia
294	74	6.7	290	2	Q8AUZ0	Q8auz0	tyrannochro
295	74	6.7	290	2	Q8AUZ1	Q8auz1	pseudotroph
296	74	6.7	290	2	Q8AUZ2	Q8auz2	cynotilapia
297	74	6.7	290	2	Q8AUZ4	Q8auz4	aulonocara
298	74	6.7	311	2	Q8LWY4	Q8lwy4	laminaria d
299	74	6.7	357	1	OPSR_CARAU	P32313	carassius a
300	74	6.7	357	2	Q98UH7	Q98uh7	cyprinus ca
301	74	6.7	357	2	Q68YX7	Q68yx7	haplochromi
302	74	6.7	357	2	Q78C19	Q78c19	metriaclima
303	74	6.7	357	2	Q9I853	Q9i853	dimidiochro
304	74	6.7	357	2	Q9I857	Q9i857	labeotrophe
305	74	6.7	371	2	Q73JG1	Q73jg1	treponema d
306	74	6.7	494	2	Q8DWV1	Q8dwv1	streptococc
307	74	6.7	510	2	Q74ID6	Q74id6	lactobacill
308	74	6.7	546	2	Q6L0W9	Q6l0w9	picrophilus
309	74	6.7	589	2	Q9R9H8	Q9r9h8	bacillus su
310	74	6.7	589	2	O06988	O06988	bacillus su
311	74	6.7	626	2	Q90880	Q90880	gallus gall
312	74	6.7	626	2	Q98922	Q98922	gallus gall
313	74	6.7	681	2	Q6ZFS6	Q6zfs6	oryza sativ
314	74	6.7	925	2	Q7YYJ8	Q7yyj8	cryptospori
315	74	6.7	1056	2	Q8P875	Q8p875	xanthomonas
316	74	6.7	1059	2	Q8CHF0	Q8chf0	mus musculu
317	74	6.7	1115	2	Q751K4	Q751k4	ashbya goss
318	73.5	6.7	94	1	FXY6_MOUSE	Q9d164	mus musculu
319	73.5	6.7	94	1	FXY6_RAT	Q91xv6	rattus norv
320	73.5	6.7	154	2	Q9V4K8	Q9v4k8	drosophila
321	73.5	6.7	229	2	Q7Z546	Q7z546	homo sapien
322	73.5	6.7	278	2	Q87IR5	Q87ir5	vibrio para
323	73.5	6.7	280	2	Q9AI49	Q9ai49	burkholderi
324	73.5	6.7	301	2	Q8EVY9	Q8evy9	mycoplasma
325	73.5	6.7	307	2	Q645Y3	Q645y3	gorilla gor
326	73.5	6.7	321	2	Q8Y7D0	Q8y7d0	listeria mo
327	73.5	6.7	349	2	Q8HX41	Q8hx41	salmo salar
328	73.5	6.7	383	2	Q62HF3	Q62hf3	burkholderi
329	73.5	6.7	465	1	FTH1_YEAST	P38310	saccharomyc
330	73.5	6.7	485	2	O10430	O10430	junin arena
331	73.5	6.7	485	2	Q642U8	Q642u8	junin arena
332	73.5	6.7	488	2	Q9GPA2	Q9gpa2	caenorhabdi
333	73.5	6.7	553	2	Q9MZL1	Q9mzl1	macaca mula
334	73.5	6.7	563	2	Q8FUB5	Q8fub5	corynebacte
335	73.5	6.7	578	2	Q83EB6	Q83eb6	coxiella bu
336	73.5	6.7	624	2	Q9SHN0	Q9shn0	arabidopsis
337	73.5	6.7	630	1	MUC1_MOUSE	Q02496	mus musculu
338	73.5	6.7	636	2	Q22040	Q22040	caenorhabdi
339	73.5	6.7	656	2	Q8TWM1	Q8twm1	methanopyru
340	73.5	6.7	782	2	O37353	O37353	lymantria d
341	73.5	6.7	783	2	Q9YMR1	Q9ymr1	lymantria d
342	73.5	6.7	785	1	CAD7_HUMAN	Q9ulb5	homo sapien
343	73.5	6.7	796	1	CADB_MOUSE	P55288	mus musculu
344	73.5	6.7	796	2	Q8C7Q6	Q8c7q6	mus musculu
345	73.5	6.7	857	2	Q6B3P0	Q6b3p0	brachydanio
346	73.5	6.7	1025	2	Q9DEU1	Q9deu1	brachydanio
347	73.5	6.7	1056	2	Q8PJN1	Q8pjn1	xanthomonas
348	73.5	6.7	1166	2	O96219	O96219	plasmodium
349	73.5	6.7	1179	2	Q7Z0L7	Q7z017	aedes aegyp
350	73.5	6.7	1179	2	Q9NCQ0	Q9ncq0	aedes aegyp
351	73.5	6.7	1188	2	Q8EJ91	Q8ej91	shewanella
352	73.5	6.7	1213	1	JAG3_BRARE	Q90y54	brachydanio
353	73.5	6.7	1721	2	Q6L450	Q6l450	solanum dem
354	73.5	6.7	1889	2	Q7Q0X2	Q7q0x2	anopheles g
355	73.5	6.7	2573	2	Q6L432	Q6l432	solanum dem
356	73.5	6.7	3350	2	Q8QVE1	Q8qve1	tamana bat
357	73.5	6.7	5054	2	Q7RPJ1	Q7rpj1	plasmodium
358	73	6.6	264	2	Q7Q5X1	Q7q5x1	anopheles g
359	73	6.6	290	2	Q8AUZ3	Q8auz3	aulonocara
360	73	6.6	290	2	Q8AUZ9	Q8auz9	gaurochromi
361	73	6.6	290	2	Q8AV01	Q8av01	paralabidoc
362	73	6.6	290	2	Q8AV02	Q8av02	paralabidoc
363	73	6.6	302	2	Q9WW83	Q9ww83	lactococcus
364	73	6.6	304	2	Q8U937	Q8u937	agrobacteri
365	73	6.6	315	2	Q9ZC71	Q9zc71	yersinia pe
366	73	6.6	326	2	Q7X9Q7	Q7x9q7	cucumis mel
367	73	6.6	343	2	Q81UZ5	Q81uz5	bacillus an
368	73	6.6	357	2	Q7T2U3	Q7t2u3	lucania goo
369	73	6.6	357	2	Q9I9I5	Q9i9i5	oreochromis
370	73	6.6	371	2	Q9SE64	Q9se64	dumasia vil
371	73	6.6	374	2	Q6I377	Q6i377	bacillus an
372	73	6.6	374	2	Q63FT6	Q63ft6	bacillus ce
373	73	6.6	374	2	Q73DD3	Q73dd3	bacillus ce
374	73	6.6	374	2	Q6HNA5	Q6hna5	bacillus th
375	73	6.6	381	2	Q30428	Q30428	canis famil
376	73	6.6	415	2	Q813R3	Q813r3	bacillus ce
377	73	6.6	512	1	SYM_MYCGE	P47267	mycoplasma
378	73	6.6	673	2	Q23706	Q23706	carcinus ma
379	73	6.6	777	2	Q8A9F3	Q8a9f3	bacteroides
380	73	6.6	780	2	Q06271	Q06271	xenopus lae
381	73	6.6	1006	2	O96608	O96608	trypanosoma
382	73	6.6	1181	1	ITA2_HUMAN	P17301	homo sapien
383	73	6.6	1244	2	Q6FNZ1	Q6fnz1	candida gla
384	73	6.6	1250	2	Q86RA5	Q86ra5	drosophila
385	73	6.6	2344	2	Q89273	Q89273	rabbit hemo
386	73	6.6	5010	2	Q81CV2	Q81cv2	bacillus ce
387	72.5	6.6	144	2	Q6QGY4	Q6qgy4	citrullus l
388	72.5	6.6	185	2	Q6AGJ7	Q6agj7	leifsonia x
389	72.5	6.6	193	2	Q60551	Q60551	mesocricetu
390	72.5	6.6	291	2	Q8C1X2	Q8c1x2	mus musculu
391	72.5	6.6	299	1	CD80_RABIT	P42070	oryctolagus
392	72.5	6.6	335	2	P79607	P79607	phoca vitul
393	72.5	6.6	426	2	Q9CLH8	Q9clh8	pasteurella
394	72.5	6.6	440	1	HEM1_HELHP	Q7vff1	helicobacte
395	72.5	6.6	541	2	Q9DSJ0	Q9dsj0	human immun
396	72.5	6.6	682	2	Q9M3E5	Q9m3e5	arabidopsis

397	72.5	6.6	905	2	Q7N649	Q7n649	photorhabdu
398	72.5	6.6	913	2	Q86AX0	Q86ax0	dictyosteli
399	72.5	6.6	1035	2	Q6QAF3	Q6qaf3	brachydanio
400	72.5	6.6	1050	1	ITA5_XENLA	Q06274	xenopus lae
401	72.5	6.6	1222	2	Q8MY76	Q8my76	sexostrea e
402	72.5	6.6	2873	1	RBP1_PLAVB	Q00798	plasmodium
403	72	6.5	93	2	Q641S5	Q641s5	xenopus lae
404	72	6.5	290	2	Q8AUI9	Q8aui9	neochromis
405	72	6.5	290	2	Q8AUJ0	Q8auj0	haplochromi
406	72	6.5	290	2	Q8AUP9	Q8aup9	haplochromi
407	72	6.5	290	2	Q8AUR5	Q8aur5	astatoreoch
408	72	6.5	290	2	Q8AUZ5	Q8auz5	haplochromi
409	72	6.5	290	2	Q8AV00	Q8av00	paralabidoc
410	72	6.5	290	2	Q8AV05	Q8av05	yssichromis
411	72	6.5	302	2	Q64SU7	Q64su7	bacteroides
412	72	6.5	361	2	Q86T72	Q86t72	homo sapien
413	72	6.5	374	2	Q93N69	Q93n69	bacillus ce
414	72	6.5	379	2	Q7Q0J1	Q7q0j1	anopheles g
415	72	6.5	439	2	Q8ZPD1	Q8zpd1	salmonella
416	72	6.5	479	2	Q8M9Q3	Q8m9q3	globularia
417	72	6.5	485	2	Q8ZSH2	Q8zsh2	anabaena sp
418	72	6.5	486	2	Q9GYU4	Q9gyu4	sepia offic
419	72	6.5	518	2	Q6C3L1	Q6c311	yarrowia li
420	72	6.5	526	2	O74292	O74292	gibberella
421	72	6.5	543	2	O16749	O16749	caenorhabdi
422	72	6.5	588	2	Q9VGA8	Q9vga8	drosophila
423	72	6.5	591	2	Q6BKU7	Q6bku7	debaryomyce
424	72	6.5	674	2	Q84ET8	Q84et8	pseudomonas
425	72	6.5	760	2	Q9FC45	Q9fc45	streptomyce
426	72	6.5	787	2	Q6I651	Q6i651	oryza sativ
427	72	6.5	792	1	CADB_CHICK	O93319	gallus gall
428	72	6.5	865	2	Q7EZ33	Q7ez33	oryza sativ
429	72	6.5	877	2	Q8S6D6	Q8s6d6	oryza sativ
430	72	6.5	1007	1	GRD2_HUMAN	O43424	homo sapien
431	72	6.5	1036	1	Y414_MYCGE	P47653	mycoplasma
432	72	6.5	1106	1	ITA7_RAT	Q63258	rattus norv
433	72	6.5	1293	2	Q9U1Q9	Q9u1q9	caenorhabdi
434	72	6.5	1436	2	Q96ZJ5	Q96zj5	sulfolobus
435	72	6.5	1795	2	Q6MUJ8	Q6muj8	mycoplasma
436	72	6.5	2344	2	Q9EMC2	Q9emc2	rabbit hemo
437	72	6.5	3251	2	Q8K4E0	Q8k4e0	mus musculu
438	72	6.5	5005	2	Q9PPZ5	Q9ppz5	ureaplasma
439	71.5	6.5	97	2	Q6S7D6	Q6s7d6	sus scrofa
440	71.5	6.5	207	2	Q6LYY0	Q6lyy0	methanococc
441	71.5	6.5	258	2	Q67JM0	Q67jm0	symbiobacte
442	71.5	6.5	264	2	Q7Z547	Q7z547	homo sapien
443	71.5	6.5	331	1	ISPH_LISMO	P58676	listeria mo
444	71.5	6.5	338	2	Q95509	Q95509	leopardus p
445	71.5	6.5	338	2	Q95512	Q95512	leopardus p
446	71.5	6.5	364	2	Q8HX60	Q8hx60	sus scrofa
447	71.5	6.5	375	2	Q65280	Q65280	african swi
448	71.5	6.5	453	2	O84414	O84414	chlamydia t
449	71.5	6.5	506	2	Q7YKQ9	Q7ykq9	avicennia g
450	71.5	6.5	512	2	Q6FXF6	Q6fxf6	candida gla
451	71.5	6.5	549	2	Q9D006	Q9d006	mus musculu
452	71.5	6.5	549	2	Q9JLB9	Q9jlb9	mus musculu
453	71.5	6.5	620	2	Q74HL2	Q74hl2	lactobacill
454	71.5	6.5	640	2	Q8LI83	Q8li83	oryza sativ
455	71.5	6.5	676	1	MUC1_MESAU	Q60528	mesocricetu
456	71.5	6.5	692	2	Q9SB75	Q9sb75	arabidopsis
457	71.5	6.5	713	2	Q9VRE0	Q9vre0	drosophila
458	71.5	6.5	718	2	Q93ZR5	Q93zr5	arabidopsis
459	71.5	6.5	718	2	Q9LSR8	Q9lsr8	arabidopsis
460	71.5	6.5	785	2	Q67G09	Q67g09	mus musculu
461	71.5	6.5	785	2	Q8BM92	Q8bm92	mus musculu
462	71.5	6.5	796	1	CADB_HUMAN	P55287	homo sapien
463	71.5	6.5	796	2	Q96CZ9	Q96cz9	homo sapien
464	71.5	6.5	837	2	Q6BFW3	Q6bfw3	paramecium
465	71.5	6.5	879	2	O81066	O81066	arabidopsis
466	71.5	6.5	936	2	O25141	O25141	helicobacte
467	71.5	6.5	1038	2	Q8YSN0	Q8ysn0	anabaena sp
468	71.5	6.5	1139	1	INA1_CAEEL	Q03600	caenorhabdi
469	71.5	6.5	1330	2	Q84QR0	Q84qr0	oryza sativ
470	71	6.4	98	2	Q8E2T7	Q8e2t7	streptococc
471	71	6.4	118	2	Q83GY2	Q83gy2	tropheryma
472	71	6.4	157	2	Q66WB3	Q66wb3	hesperia co
473	71	6.4	157	2	Q66WB9	Q66wb9	hesperia co
474	71	6.4	157	2	Q66WC6	Q66wc6	hesperia co
475	71	6.4	183	2	Q96MQ8	Q96mq8	homo sapien
476	71	6.4	183	2	Q9TQU9	Q9tqu9	bos taurus
477	71	6.4	225	2	Q8L270	Q8l270	proteus vul
478	71	6.4	235	2	Q8WYN2	Q8wyn2	homo sapien
479	71	6.4	250	2	Q72ED8	Q72ed8	desulfovibr
480	71	6.4	262	2	Q23480	Q23480	caenorhabdi
481	71	6.4	274	2	Q92LM1	Q92lm1	rhizobium m
482	71	6.4	290	2	Q8AUT5	Q8aut5	yssichromis
483	71	6.4	290	2	Q8AV03	Q8av03	yssichromis
484	71	6.4	292	2	Q8WNW1	Q8wnw1	bos taurus
485	71	6.4	292	2	Q9GKE0	Q9gke0	bos taurus
486	71	6.4	303	2	Q7ZXR4	Q7zxr4	xenopus lae
487	71	6.4	305	2	Q8EQS0	Q8eqs0	oceanobacil
488	71	6.4	306	2	Q81M30	Q81m30	bacillus an
489	71	6.4	307	2	Q7R3F7	Q7r3f7	giardia lam
490	71	6.4	316	2	Q9F3S9	Q9f3s9	rhodothermu
491	71	6.4	321	2	Q92C01	Q92c01	listeria in
492	71	6.4	325	2	Q924S3	Q924s3	rattus norv
493	71	6.4	326	1	TGL2_YEAST	P54857	saccharomyc
494	71	6.4	326	2	Q6Q5U9	Q6q5u9	saccharomyc
495	71	6.4	327	2	Q9GEZ3	Q9gez3	gymnosteris
496	71	6.4	335	2	Q8N9J3	Q8n9j3	homo sapien
497	71	6.4	335	2	Q9GEZ1	Q9gez1	ipomopsis a
498	71	6.4	336	2	Q8JHI2	Q8jhi2	brachydanio
499	71	6.4	338	2	Q9H5A4	Q9h5a4	homo sapien
500	71	6.4	342	2	Q8G2I3	Q8g2i3	brucella su
501	71	6.4	342	2	Q7ZXJ4	Q7zxj4	xenopus lae
502	71	6.4	347	2	Q658M7	Q658m7	homo sapien
503	71	6.4	358	2	Q8IHG8	Q8ihg8	drosophila
504	71	6.4	358	2	Q8MLK8	Q8mlk8	drosophila
505	71	6.4	366	1	CD44_BOVIN	Q29423	bos taurus
506	71	6.4	366	1	YNI0_YEAST	P53938	saccharomyc
507	71	6.4	389	2	Q8A1Z3	Q8a1z3	bacteroides
508	71	6.4	423	2	Q8XIY7	Q8xiy7	clostridium
509	71	6.4	463	2	Q68AX5	Q68ax5	fugu rubrip
510	71	6.4	463	2	Q68AX6	Q68ax6	fugu rubrip
511	71	6.4	470	2	Q9H5A6	Q9h5a6	homo sapien
512	71	6.4	482	2	Q70IB7	Q70ib7	calceolaria
513	71	6.4	489	2	Q8Y6R6	Q8y6r6	listeria mo
514	71	6.4	489	2	Q92B92	Q92b92	listeria in
515	71	6.4	493	2	Q86Z27	Q86z27	homo sapien
516	71	6.4	499	2	Q8BYS0	Q8bys0	mus musculu
517	71	6.4	507	2	Q6A152	Q6a152	mus musculu
518	71	6.4	508	2	Q8FD36	Q8fd36	escherichia
519	71	6.4	513	2	Q9NKV9	Q9nkv9	drosophila
520	71	6.4	514	2	Q62913	Q62913	rattus norv
521	71	6.4	533	2	Q9YCP8	Q9ycp8	aeropyrum p
522	71	6.4	548	2	Q6AXQ6	Q6axq6	rattus norv
523	71	6.4	560	1	NMB_HUMAN	Q14956	homo sapien
524	71	6.4	572	2	Q8N1A1	Q8n1a1	homo sapien
525	71	6.4	572	2	Q6UVX1	Q6uvx1	homo sapien
526	71	6.4	627	2	Q9ZW09	Q9zw09	arabidopsis
527	71	6.4	676	2	Q9H5A7	Q9h5a7	homo sapien
528	71	6.4	685	1	ATKB_CLOAB	O32328	clostridium
529	71	6.4	717	2	Q8I4R9	Q8i4r9	plasmodium
530	71	6.4	719	2	Q9H5A5	Q9h5a5	homo sapien
531	71	6.4	742	1	CD44_HUMAN	P16070	h cd44 anti
532	71	6.4	742	2	Q9UJ36	Q9uj36	homo sapien
533	71	6.4	826	2	Q97J76	Q97j76	clostridium
534	71	6.4	836	2	Q6DCD5	Q6dcd5	xenopus lae
535	71	6.4	894	2	Q7PMF1	Q7pmf1	anopheles g
536	71	6.4	1009	2	Q98SL3	Q98sl3	electrophor
537	71	6.4	1037	2	Q7M075	Q7m075	rattus sp.
538	71	6.4	1097	1	PGDR_RAT	Q05030	rattus norv
539	71	6.4	1238	1	PTPJ_MOUSE	Q64455	mus musculu
540	71	6.4	1238	2	Q8K3Q2	Q8k3q2	mus musculu
541	71	6.4	1238	2	Q8CIW9	Q8ciw9	mus musculu
542	71	6.4	1278	2	Q7RMJ9	Q7rmj9	plasmodium

543	71	6.4	1415	2	Q8MJ16	Q8mj16	bos taurus
544	71	6.4	1427	2	Q8VIB7	Q8vib7	mesocricetu
545	71	6.4	1429	1	ATRN_HUMAN	O75882	homo sapien
546	71	6.4	1432	2	Q99J86	Q99j86	rattus norv
547	71	6.4	1501	2	Q7TT17	Q7tt17	mus musculu
548	71	6.4	1501	2	Q9QW00	Q9qw00	rattus sp.
549	71	6.4	1502	2	Q9UM81	Q9um81	homo sapien
550	71	6.4	1863	2	Q64605	Q64605	rattus norv
551	71	6.4	1904	2	Q64699	Q64699	mus musculu
552	71	6.4	1948	1	PTNS_HUMAN	Q13332	homo sapien
553	71	6.4	2344	1	POLN_RHDV	P27410	r non-struc
554	71	6.4	2699	2	Q7RLQ0	Q7rlq0	plasmodium
555	71	6.4	3699	2	Q9HFE8	Q9hfe8	schizosacch
556	71	6.4	5138	2	Q9ZW94	Q9zw94	arabidopsis
557	70.5	6.4	71	1	DMS4_PACDA	O93454	pachymedusa
558	70.5	6.4	154	2	Q860J2	Q860j2	giraffa cam
559	70.5	6.4	157	2	Q7XV56	Q7xv56	oryza sativ
560	70.5	6.4	199	2	Q8CBS5	Q8cbs5	m mus muscu
561	70.5	6.4	224	2	Q8CBU5	Q8cbu5	m mus muscu
562	70.5	6.4	246	2	Q81P02	Q81p02	bacillus an
563	70.5	6.4	269	2	Q94F24	Q94f24	arabidopsis
564	70.5	6.4	291	2	Q8K1A5	Q8k1a5	m d7ertd743
565	70.5	6.4	302	2	Q8KJR9	Q8kjr9	lactobacill
566	70.5	6.4	305	2	Q6HX74	Q6hx74	bacillus an
567	70.5	6.4	307	2	Q646B2	Q646b2	pan troglod
568	70.5	6.4	310	2	Q8BEI8	Q8bei8	vaccinia vi
569	70.5	6.4	332	2	Q7U8V4	Q7u8v4	synechococc
570	70.5	6.4	370	2	Q6HH96	Q6hh96	bacillus th
571	70.5	6.4	373	2	Q8JSN9	Q8jsn9	african swi
572	70.5	6.4	373	2	Q6JHU1	Q6jhu1	african swi
573	70.5	6.4	374	2	Q88DL9	Q88dl9	pseudomonas
574	70.5	6.4	422	2	Q9HKX6	Q9hkx6	thermoplasm
575	70.5	6.4	431	1	TOLB_WIGBR	Q8d2e2	wiggleswort
576	70.5	6.4	438	2	Q8E8M9	Q8e8m9	shewanella
577	70.5	6.4	467	2	Q8H199	Q8h199	arabidopsis
578	70.5	6.4	478	2	Q70IC0	Q70ic0	calceolaria
579	70.5	6.4	516	2	O48924	O48924	glycine max
580	70.5	6.4	552	2	Q756T8	Q756t8	ashbya goss
581	70.5	6.4	561	2	Q9CKX7	Q9ckx7	pasteurella
582	70.5	6.4	582	2	Q8WPH4	Q8wph4	drosophila
583	70.5	6.4	584	2	Q22629	Q22629	caenorhabdi
584	70.5	6.4	617	2	Q95ZX6	Q95zx6	caenorhabdi
585	70.5	6.4	736	2	Q6ZIQ8	Q6ziq8	oryza sativ
586	70.5	6.4	783	2	Q7R5Y0	Q7r5y0	giardia lam
587	70.5	6.4	783	2	Q86LL3	Q86ll3	giardia lam
588	70.5	6.4	801	1	CADK_HUMAN	Q9hbt6	homo sapien
589	70.5	6.4	837	2	Q86G85	Q86g85	pseudoplusi
590	70.5	6.4	900	2	O65474	O65474	arabidopsis
591	70.5	6.4	999	2	Q8MQP4	Q8mqp4	drosophila
592	70.5	6.4	1027	1	A1A1_CATCO	P25489	catostomus
593	70.5	6.4	1049	2	Q66QA5	Q66qa5	oryza sativ
594	70.5	6.4	1121	2	O61931	O61931	caenorhabdi
595	70.5	6.4	1166	2	Q7RIF6	Q7rif6	plasmodium
596	70.5	6.4	1167	2	O88341	O88341	rattus norv
597	70.5	6.4	1171	2	Q9VTW8	Q9vtw8	drosophila
598	70.5	6.4	1173	1	ATC2_YEAST	P38929	saccharomyc
599	70.5	6.4	1203	2	Q9NGZ4	Q9ngz4	drosophila
600	70.5	6.4	1291	2	Q9VIF9	Q9vif9	drosophila
601	70.5	6.4	1788	2	Q9IAJ0	Q9iaj0	xenopus lae
602	70.5	6.4	2607	2	Q6L4J5	Q6l4j5	solanum dem
603	70.5	6.4	2672	1	GCN1_YEAST	P33892	saccharomyc
604	70	6.4	94	2	Q9K3M7	Q9k3m7	streptomyce
605	70	6.4	122	2	Q8C9G7	Q8c9g7	mus musculu
606	70	6.4	183	2	Q9TQU8	Q9tqu8	bos indicus
607	70	6.4	183	2	Q9TTR5	Q9ttr5	bos taurus
608	70	6.4	264	2	Q9YEK5	Q9yek5	aeropyrum p
609	70	6.4	276	2	Q6P0R7	Q6p0r7	brachydanio
610	70	6.4	280	2	Q8K3G1	Q8k3g1	rattus norv
611	70	6.4	302	2	Q6I7J2	Q6i7j2	lactobacill
612	70	6.4	304	2	Q89X91	Q89x91	bradyrhizob
613	70	6.4	306	2	Q634Y3	Q634y3	bacillus ce
614	70	6.4	306	2	Q730Z2	Q730z2	bacillus ce
615	70	6.4	310	1	FTSX_HAEIN	P44872	haemophilus
616	70	6.4	331	2	Q7V5T6	Q7v5t6	prochloroco
617	70	6.4	333	2	O44603	O44603	caenorhabdi
618	70	6.4	335	2	Q7YW74	Q7yw74	rhipicephal
619	70	6.4	341	2	Q99XH9	Q99xh9	streptococc
620	70	6.4	342	2	Q8TL28	Q8tl28	methanosarc
621	70	6.4	346	2	Q8HK31	Q8hk31	xiphorhynch
622	70	6.4	346	2	Q8HK52	Q8hk52	xiphorhynch
623	70	6.4	354	2	Q65U34	Q65u34	mannheimia
624	70	6.4	362	1	VP61_MRDV	P22119	maize rough
625	70	6.4	386	2	Q6HLX8	Q6hlx8	bacillus th
626	70	6.4	396	2	Q6ZW42	Q6zw42	homo sapien
627	70	6.4	402	2	Q89501	Q89501	african swi
628	70	6.4	428	2	Q821Z4	Q821z4	chlamydophi
629	70	6.4	470	2	Q65J05	Q65j05	bacillus li
630	70	6.4	488	2	Q73G56	Q73g56	wolbachia p
631	70	6.4	489	1	PT94_YEAST	P07390	saccharomyc
632	70	6.4	492	2	Q26580	Q26580	schistosoma
633	70	6.4	544	2	Q9CF49	Q9cf49	lactococcus
634	70	6.4	556	2	Q7VHM0	Q7vhm0	helicobacte
635	70	6.4	560	2	Q7QW34	Q7qw34	giardia lam
636	70	6.4	644	2	Q6MYU2	Q6myu2	aspergillus
637	70	6.4	678	2	Q9VBV7	Q9vbv7	drosophila
638	70	6.4	683	2	Q6ZFS5	Q6zfs5	oryza sativ
639	70	6.4	701	2	Q7PS25	Q7ps25	anopheles g
640	70	6.4	745	2	Q8WST7	Q8wst7	halocynthia
641	70	6.4	753	2	Q845W1	Q845w1	burkholderi
642	70	6.4	780	2	Q7KQS9	Q7kqs9	drosophila
643	70	6.4	801	2	Q9Z0M3	Q9z0m3	mus musculu
644	70	6.4	813	2	Q64C97	Q64c97	uncultured
645	70	6.4	831	2	Q755V1	Q755v1	ashbya goss
646	70	6.4	921	2	Q8QS33	Q8qs33	pongine her
647	70	6.4	1023	2	Q7ZYV1	Q7zyv1	anas platyr
648	70	6.4	1039	1	ITAB_HUMAN	P08514	homo sapien
649	70	6.4	1073	2	Q70GQ8	Q70gq8	drosophila
650	70	6.4	1078	2	Q7SHS0	Q7shs0	neurospora
651	70	6.4	1178	1	ITA2_MOUSE	Q62469	mus musculu
652	70	6.4	1178	2	Q6P1C7	Q6p1c7	mus musculu
653	70	6.4	1212	2	O42347	O42347	gallus gall
654	70	6.4	1226	2	Q9V4U3	Q9v4u3	drosophila
655	70	6.4	1264	2	Q9V4U4	Q9v4u4	drosophila
656	70	6.4	1357	2	Q7SF20	Q7sf20	neurospora
657	70	6.4	1635	2	O17368	O17368	caenorhabdi
658	70	6.4	1636	1	YN37_YEAST	P48563	saccharomyc
659	70	6.4	1721	2	Q93547	Q93547	caenorhabdi
660	70	6.4	2168	1	POLG_PEV9U	O41174	p genome po
661	70	6.4	2168	2	Q8QUZ8	Q8quz8	porcine ent
662	70	6.4	20925	2	Q8NJX1	Q8njx1	trichoderma
663	69.5	6.3	108	2	Q6S7D8	Q6s7d8	sus scrofa
664	69.5	6.3	215	2	Q6ZSK9	Q6zsk9	homo sapien
665	69.5	6.3	222	2	Q9I7D5	Q9i7d5	drosophila
666	69.5	6.3	237	2	Q6BCB6	Q6bcb6	trionyx sin
667	69.5	6.3	244	2	Q720M5	Q720m5	listeria mo
668	69.5	6.3	246	2	Q8BTG9	Q8btg9	mus musculu
669	69.5	6.3	262	2	Q8RTW4	Q8rtw4	uncultured
670	69.5	6.3	267	2	Q9SHW0	Q9shw0	arabidopsis
671	69.5	6.3	270	2	Q9D8G2	Q9d8g2	mus musculu
672	69.5	6.3	273	2	Q6IVG2	Q6ivg2	mus musculu
673	69.5	6.3	281	2	P97300	P97300	mus musculu
674	69.5	6.3	290	2	Q9EP73	Q9ep73	mus musculu
675	69.5	6.3	292	2	Q97QE8	Q97qe8	streptococc
676	69.5	6.3	296	2	Q8DPI5	Q8dpi5	streptococc
677	69.5	6.3	297	2	Q6C5D7	Q6c5d7	yarrowia li
678	69.5	6.3	300	2	Q8BEK0	Q8bek0	cowpox viru
679	69.5	6.3	303	2	Q92RX2	Q92rx2	rhizobium m
680	69.5	6.3	307	2	Q646C7	Q646c7	pan paniscu
681	69.5	6.3	310	2	Q8BEI7	Q8bei7	vaccinia vi
682	69.5	6.3	315	2	Q8U6V9	Q8u6v9	agrobacteri
683	69.5	6.3	323	2	Q6F222	Q6f222	mesoplasma
684	69.5	6.3	334	2	Q6TXS0	Q6txs0	cherax dest
685	69.5	6.3	348	1	VIPL_HUMAN	Q9h0v9	homo sapien
686	69.5	6.3	351	1	FXI1_HUMAN	Q12951	homo sapien
687	69.5	6.3	359	2	Q63HN6	Q63hn6	homo sapien
688	69.5	6.3	361	2	Q8HX64	Q8hx64	sus scrofa

689	69.5	6.3	361	2	Q8MHT5	Q8mht5 sus scrofa
690	69.5	6.3	361	2	Q8SPB9	Q8spb9 sus scrofa
691	69.5	6.3	395	2	Q9FKY4	Q9fky4 arabidopsis
692	69.5	6.3	406	2	Q7PPN3	Q7ppn3 anopheles g
693	69.5	6.3	412	2	Q63611	Q63611 rattus norv
694	69.5	6.3	412	2	Q9R1E1	Q9r1e1 rattus norv
695	69.5	6.3	427	2	Q8CI68	Q8ci68 mus musculu
696	69.5	6.3	446	2	Q6CQ08	Q6cq08 kluyveromyc
697	69.5	6.3	446	2	Q9Y849	Q9y849 kluyveromyc
698	69.5	6.3	450	2	Q74CN3	Q74cn3 geobacter s
699	69.5	6.3	452	2	Q8SXY5	Q8sxy5 drosophila
700	69.5	6.3	455	2	Q6AFY9	Q6afy9 leifsonia x
701	69.5	6.3	479	2	Q7A9A2	Q7a9a2 escherichia
702	69.5	6.3	481	2	Q8X8A5	Q8x8a5 escherichia
703	69.5	6.3	490	2	Q94CC5	Q94cc5 arabidopsis
704	69.5	6.3	552	2	Q67QA3	Q67qa3 symbiobacte
705	69.5	6.3	555	2	Q69HR1	Q69hr1 ciona intes
706	69.5	6.3	623	2	Q9HIE1	Q9hie1 thermoplasm
707	69.5	6.3	679	2	Q7R5N8	Q7r5n8 giardia lam
708	69.5	6.3	708	2	O87239	O87239 lactococcus
709	69.5	6.3	746	2	Q6DIR2	Q6dir2 xenopus tro
710	69.5	6.3	795	2	Q6C6E5	Q6c6e5 yarrowia li
711	69.5	6.3	882	2	Q9TZL6	Q9tzl6 caenorhabdi
712	69.5	6.3	900	2	O74925	O74925 schizosacch
713	69.5	6.3	956	2	Q8BMF5	Q8bmf5 mus musculu
714	69.5	6.3	1021	2	Q7XKA3	Q7xka3 oryza sativ
715	69.5	6.3	1036	1	ATHL_RAT	P54708 rattus norv
716	69.5	6.3	1036	2	Q9TUN6	Q9tun6 sus scrofa
717	69.5	6.3	1069	1	PCH7_HUMAN	O60245 homo sapien
718	69.5	6.3	1560	2	Q18291	Q18291 caenorhabdi
719	69.5	6.3	2283	1	DPOE_MOUSE	Q9wvf7 mus musculu
720	69.5	6.3	2283	2	Q80XH7	Q80xh7 mus musculu
721	69	6.3	157	2	Q7QAU5	Q7qau5 anopheles g
722	69	6.3	220	2	Q8KFX6	Q8kfx6 chlorobium
723	69	6.3	224	2	Q932N1	Q932n1 staphylococ
724	69	6.3	231	2	Q9HUP0	Q9hup0 pseudomonas
725	69	6.3	275	2	Q9RK73	Q9rk73 streptomyce
726	69	6.3	305	2	Q98M70	Q98m70 rhizobium l
727	69	6.3	321	2	Q71ZW9	Q71zw9 listeria mo
728	69	6.3	332	2	Q6SL18	Q6sl18 pollicipes
729	69	6.3	339	2	Q9GJK0	Q9gjk0 salmo trutt
730	69	6.3	345	2	Q922I5	Q922i5 mus musculu
731	69	6.3	347	1	VIPL_MOUSE	P59481 mus musculu
732	69	6.3	350	2	O93556	O93556 carassius a
733	69	6.3	358	2	Q95559	Q95559 peromyscus
734	69	6.3	369	1	OPSR_ANOCA	P41592 anolis caro
735	69	6.3	372	2	Q9D299	Q9d299 mus musculu
736	69	6.3	390	2	Q8KR52	Q8kr52 escherichia
737	69	6.3	393	2	Q7RI96	Q7ri96 plasmodium
738	69	6.3	394	2	Q8IK51	Q8ik51 plasmodium
739	69	6.3	395	2	Q8CGD8	Q8cgd8 mus musculu
740	69	6.3	398	2	Q90ZL8	Q90zl8 anas platyr
741	69	6.3	401	2	Q9KRK6	Q9krk6 vibrio chol
742	69	6.3	433	2	Q8A897	Q8a897 bacteroides
743	69	6.3	454	2	Q86ZD2	Q86zd2 fusarium ox
744	69	6.3	456	2	Q643C2	Q643c2 streptomyce
745	69	6.3	479	2	Q93JF0	Q93jf0 streptomyce
746	69	6.3	482	2	Q70IB8	Q70ib8 calceolaria
747	69	6.3	495	2	Q7VLI6	Q7vli6 haemophilus
748	69	6.3	495	2	Q9APM3	Q9apm3 haemophilus
749	69	6.3	501	2	Q6DB53	Q6db53 erwinia car
750	69	6.3	512	2	Q95K28	Q95k28 macaca fasc
751	69	6.3	569	2	Q73VL3	Q73vl3 mycobacteri
752	69	6.3	616	1	NDVA_RHIME	P18767 rhizobium m
753	69	6.3	645	2	Q6BPF8	Q6bpf8 debaryomyce
754	69	6.3	666	2	Q8MT84	Q8mt84 drosophila
755	69	6.3	666	2	Q9V3S9	Q9v3s9 drosophila
756	69	6.3	688	2	Q6ZFT2	Q6zft2 oryza sativ
757	69	6.3	697	2	Q8NC72	Q8nc72 homo sapien
758	69	6.3	707	2	Q95JR7	Q95jr7 macaca fasc
759	69	6.3	723	2	Q6ZW32	Q6zw32 homo sapien
760	69	6.3	723	2	Q7Z329	Q7z329 homo sapien
761	69	6.3	723	2	Q7Z388	Q7z388 homo sapien
762	69	6.3	728	2	Q9MAQ5	Q9maq5 arabidopsis
763	69	6.3	773	2	Q98R04	Q98r04 mycoplasma
764	69	6.3	811	1	COAT_GMDNV	Q90125 galleria me
765	69	6.3	864	2	Q6FVT1	Q6fvt1 candida gla
766	69	6.3	943	2	Q9FG43	Q9fg43 arabidopsis
767	69	6.3	996	2	P90735	P90735 caenorhabdi
768	69	6.3	996	2	Q27461	Q27461 caenorhabdi
769	69	6.3	1017	1	A1A2_CHICK	P24797 gallus gall
770	69	6.3	1059	2	Q6UXL7	Q6uxl7 homo sapien
771	69	6.3	1119	2	Q6UXM1	Q6uxm1 homo sapien
772	69	6.3	1181	1	ITA7_HUMAN	Q13683 homo sapien
773	69	6.3	1191	2	Q756U3	Q756u3 ashbya goss
774	69	6.3	1256	2	Q6BT77	Q6bt77 debaryomyce
775	69	6.3	1560	2	Q9GRX5	Q9grx5 dictyosteli
776	69	6.3	1561	2	Q9U987	Q9u987 dictyosteli
777	69	6.3	1993	2	Q7PS34	Q7ps34 anopheles g
778	69	6.3	5017	2	Q81FJ0	Q81fj0 bacillus ce
779	68.5	6.2	74	2	Q8R4P1	Q8r4p1 mus musculu
780	68.5	6.2	110	2	Q9KZQ3	Q9kzq3 streptomyce
781	68.5	6.2	116	2	Q8LBX7	Q8lbx7 arabidopsis
782	68.5	6.2	140	2	Q69M00	Q69m00 oryza sativ
783	68.5	6.2	141	2	P91181	P91181 caenorhabdi
784	68.5	6.2	179	2	Q7PQH2	Q7pqh2 anopheles g
785	68.5	6.2	248	2	O62701	O62701 sus scrofa
786	68.5	6.2	296	2	Q88IP7	Q88ip7 pseudomonas
787	68.5	6.2	304	2	Q9TQX1	Q9tqx1 canis famil
788	68.5	6.2	316	2	Q20259	Q20259 caenorhabdi
789	68.5	6.2	330	1	QUTG_EMENI	P25416 emericella
790	68.5	6.2	342	2	Q30488	Q30488 equus cabal
791	68.5	6.2	348	1	RNFD_VIBCH	Q9kt89 vibrio chol
792	68.5	6.2	360	2	Q95558	Q95558 peromyscus
793	68.5	6.2	365	2	Q93UK1	Q93uk1 burkholderi
794	68.5	6.2	383	2	Q63R65	Q63r65 burkholderi
795	68.5	6.2	397	1	C244_MOUSE	Q07763 mus musculu
796	68.5	6.2	410	2	Q7MWS8	Q7mws8 porphyromon
797	68.5	6.2	417	2	O25454	O25454 helicobacte
798	68.5	6.2	422	2	Q7ZTZ8	Q7ztz8 brachydanio
799	68.5	6.2	444	2	Q8HVW8	Q8hvw8 lantana cam
800	68.5	6.2	469	2	Q18644	Q18644 caenorhabdi
801	68.5	6.2	477	2	Q8M8X4	Q8m8x4 selago thom
802	68.5	6.2	478	2	Q70IC1	Q70ic1 calceolaria
803	68.5	6.2	483	1	PTVB_ECOLI	P32154 escherichia
804	68.5	6.2	483	2	Q7UB78	Q7ub78 shigella fl
805	68.5	6.2	485	1	VGLY_JUNIN	P26313 junin arena
806	68.5	6.2	485	2	Q83PE3	Q83pe3 shigella fl
807	68.5	6.2	485	2	O10428	O10428 junin arena
808	68.5	6.2	485	2	O10429	O10429 junin arena
809	68.5	6.2	485	2	Q6IVU3	Q6ivu3 junin arena
810	68.5	6.2	485	2	Q6UY73	Q6uy73 junin arena
811	68.5	6.2	502	2	O81915	O81915 arabidopsis
812	68.5	6.2	506	2	Q7YJZ1	Q7yjz1 harpagophyt
813	68.5	6.2	511	2	Q8YV02	Q8yv02 anabaena sp
814	68.5	6.2	522	2	O41526	O41526 canine herp
815	68.5	6.2	522	2	O91334	O91334 canine herp
816	68.5	6.2	524	2	Q72VH1	Q72vh1 leptospira
817	68.5	6.2	524	2	Q8F918	Q8f918 leptospira
818	68.5	6.2	531	2	Q91E38	Q91e38 phocid herp
819	68.5	6.2	539	2	Q7RC79	Q7rc79 plasmodium
820	68.5	6.2	543	2	Q804X8	Q804x8 gallus gall
821	68.5	6.2	559	2	Q8TPP5	Q8tpp5 methanosarc
822	68.5	6.2	564	2	Q8IS03	Q8is03 babesia bov
823	68.5	6.2	564	2	O67184	O67184 aquifex aeo
824	68.5	6.2	568	2	Q74LN5	Q74ln5 lactobacill
825	68.5	6.2	572	2	Q9VNW8	Q9vnw8 drosophila
826	68.5	6.2	589	2	Q68XF5	Q68xf5 rickettsia
827	68.5	6.2	593	2	Q8CX26	Q8cx26 streptococc
828	68.5	6.2	593	2	Q8DZ90	Q8dz90 streptococc
829	68.5	6.2	604	1	ITAB_PAPCY	P53711 papio cynoc
830	68.5	6.2	645	2	Q7RJS9	Q7rjs9 plasmodium
831	68.5	6.2	674	2	Q7XIS7	Q7xis7 oryza sativ
832	68.5	6.2	676	1	ATKB_ENTFA	Q8ku73 enterococcu
833	68.5	6.2	698	2	Q8WYI5	Q8wy15 homo sapien
834	68.5	6.2	785	2	Q6CTN0	Q6ctn0 kluyveromyc

835	68.5	6.2	798	2	Q8QGH3	Q8qgh3	gallus gall
836	68.5	6.2	798	2	Q7ZYV7	Q7zyv7	gallus gall
837	68.5	6.2	799	1	ITBN_DROME	Q27591	drosophila
838	68.5	6.2	807	2	Q21895	Q21895	caenorhabdi
839	68.5	6.2	831	2	Q69XP2	Q69xp2	oryza sativ
840	68.5	6.2	907	2	Q9FLT4	Q9flt4	arabidopsis
841	68.5	6.2	998	2	Q6GNM2	Q6gnm2	xenopus lae
842	68.5	6.2	1022	2	Q7RMR7	Q7rmr7	plasmodium
843	68.5	6.2	1025	1	ADA1_YEAST	P38065	saccharomyc
844	68.5	6.2	1041	2	Q8XQM4	Q8xqm4	ralstonia s
845	68.5	6.2	1101	2	Q39157	Q39157	arabidopsis
846	68.5	6.2	1111	2	Q9FL71	Q9fl71	arabidopsis
847	68.5	6.2	1123	2	Q9ZIB3	Q9zib3	wolinella r
848	68.5	6.2	1179	1	ITAE_HUMAN	P38570	homo sapien
849	68.5	6.2	1238	2	Q9ZIB5	Q9zib5	wolinella r
850	68.5	6.2	1269	2	Q8IJJ5	Q8ijj5	plasmodium
851	68.5	6.2	1305	2	Q757A3	Q757a3	ashbya goss
852	68.5	6.2	1710	2	Q8PSN8	Q8psn8	methanosarc
853	68.5	6.2	1776	2	Q6BMI2	Q6bmi2	debaryomyce
854	68.5	6.2	1896	2	Q9IAJ1	Q9iaj1	xenopus lae
855	68.5	6.2	1926	2	Q7S5T9	Q7s5t9	neurospora
856	68	6.2	145	2	Q9CYN8	Q9cyn8	mus musculu
857	68	6.2	153	2	Q72JJ0	Q72jj0	thermus the
858	68	6.2	168	2	Q9ZGF6	Q9zgf6	heliobacill
859	68	6.2	171	2	Q69504	Q69504	human herpe
860	68	6.2	183	2	Q6P9G4	Q6p9g4	homo sapien
861	68	6.2	190	2	Q7NAX3	Q7nax3	mycoplasma
862	68	6.2	190	2	Q80V73	Q80v73	mus musculu
863	68	6.2	217	2	Q8ERH2	Q8erh2	oceanobacil
864	68	6.2	218	2	Q7JN61	Q7jn61	dictyosteli
865	68	6.2	254	2	Q23871	Q23871	dictyosteli
866	68	6.2	267	2	Q8UEI1	Q8uei1	agrobacteri
867	68	6.2	270	2	Q99MB6	Q99mb6	mus musculu
868	68	6.2	270	2	Q9CQ56	Q9cq56	m mus muscu
869	68	6.2	275	2	Q94BJ8	Q94bj8	berberidops
870	68	6.2	284	2	Q8IM26	Q8im26	plasmodium
871	68	6.2	290	2	Q8AUP3	Q8aup3	ptyochromis
872	68	6.2	290	2	Q8AUP4	Q8aup4	haplochromi
873	68	6.2	290	2	Q8AUP5	Q8aup5	haplochromi
874	68	6.2	290	2	Q8AV04	Q8av04	yssichromis
875	68	6.2	291	2	Q6CIC6	Q6cic6	kluyveromyc
876	68	6.2	291	2	Q9MZU9	Q9mzu9	felis silve
877	68	6.2	294	2	Q8SPW3	Q8spw3	macaca fasc
878	68	6.2	297	2	Q92U54	Q92u54	rhizobium m
879	68	6.2	310	2	Q7CYK0	Q7cyk0	agrobacteri
880	68	6.2	318	1	YQHQ_BACSU	P54515	bacillus su
881	68	6.2	338	2	Q6DHD4	Q6dhd4	brachydanio
882	68	6.2	342	2	Q8YFD6	Q8yfd6	brucella me
883	68	6.2	362	1	OPSR_CHICK	P22329	gallus gall
884	68	6.2	362	2	Q8SPC0	Q8spc0	sus scrofa
885	68	6.2	397	2	Q82ZF7	Q82zf7	enterococcu
886	68	6.2	398	2	Q6D8T4	Q6d8t4	erwinia car
887	68	6.2	399	2	Q7BM45	Q7bm45	salmonella
888	68	6.2	399	2	Q9KIK0	Q9kik0	salmonella
889	68	6.2	406	2	Q7NHJ5	Q7nhj5	gloeobacter
890	68	6.2	429	2	Q17985	Q17985	caenorhabdi
891	68	6.2	433	2	O62254	O62254	caenorhabdi
892	68	6.2	452	2	Q7UA98	Q7ua98	shigella fl
893	68	6.2	454	2	Q86ZE4	Q86ze4	gibberella
894	68	6.2	472	2	Q811T8	Q811t8	mus musculu
895	68	6.2	489	2	Q97CT5	Q97ct5	thermoplasm
896	68	6.2	504	2	Q9X4B6	Q9x4b6	escherichia
897	68	6.2	510	2	Q7YKQ3	Q7ykq3	gratiola of
898	68	6.2	512	2	Q7XSP9	Q7xsp9	oryza sativ
899	68	6.2	516	2	Q8ESH6	Q8esh6	oceanobacil
900	68	6.2	538	2	Q98PI0	Q98pi0	mycoplasma
901	68	6.2	543	1	DAL5_YEAST	P15365	saccharomyc
902	68	6.2	544	2	O61196	O61196	caenorhabdi
903	68	6.2	570	2	Q9NKV8	Q9nkv8	drosophila
904	68	6.2	587	2	Q6HSF8	Q6hsf8	bacillus an
905	68	6.2	587	2	Q81L02	Q81l02	bacillus an
906	68	6.2	587	2	Q6HCU3	Q6hcu3	bacillus th
907	68	6.2	592	2	Q9N6I8	Q9n6i8	drosophila
908	68	6.2	644	2	Q95RU0	Q95ru0	drosophila
909	68	6.2	664	2	Q9SW41	Q9sw41	arabidopsis
910	68	6.2	666	2	Q9LDM5	Q9ldm5	arabidopsis
911	68	6.2	679	2	Q86QH5	Q86qh5	anopheles g
912	68	6.2	681	2	Q9FFW5	Q9ffw5	arabidopsis
913	68	6.2	691	2	O22138	O22138	arabidopsis
914	68	6.2	699	2	Q6BEN8	Q6ben8	pseudomonas
915	68	6.2	699	2	Q6QQC3	Q6qqc3	pseudomonas
916	68	6.2	699	2	Q6RBZ7	Q6rbz7	pseudomonas
917	68	6.2	699	2	Q6XDA4	Q6xda4	pseudomonas
918	68	6.2	729	1	S6AF_BOVIN	Q9xs59	bos taurus
919	68	6.2	802	2	Q6UY21	Q6uy21	homo sapien
920	68	6.2	803	2	Q8N106	Q8n106	homo sapien
921	68	6.2	878	2	Q8YV23	Q8yv23	anabaena sp
922	68	6.2	884	1	CADB_XENLA	P33152	xenopus lae
923	68	6.2	884	2	Q6NTM0	Q6ntm0	xenopus lae
924	68	6.2	905	1	CADN_XENLA	P20310	xenopus lae
925	68	6.2	923	2	Q7PWA2	Q7pwa2	anopheles g
926	68	6.2	924	2	Q8LN27	Q8ln27	oryza sativ
927	68	6.2	927	2	Q8NIQ7	Q8niq7	pichia fari
928	68	6.2	973	1	UVRA_AGRT5	Q8uf86	agrobacteri
929	68	6.2	1022	2	Q90WE7	Q90we7	carassius a
930	68	6.2	1036	2	Q7YRP8	Q7yrp8	equus cabal
931	68	6.2	1137	2	Q86W93	Q86w93	homo sapien
932	68	6.2	1221	2	Q6Y8G3	Q6y8g3	anopheles g
933	68	6.2	1223	2	Q7MEM3	Q7mem3	vibrio vuln
934	68	6.2	1227	2	Q6FNF4	Q6fnf4	candida gla
935	68	6.2	1360	2	O02006	O02006	drosophila
936	68	6.2	1818	2	Q76C94	Q76c94	drosophila
937	68	6.2	1818	2	Q76C95	Q76c95	drosophila
938	68	6.2	2268	2	Q8I4N5	Q8i4n5	plasmodium
939	68	6.2	2321	1	NTC3_HUMAN	Q9um47	homo sapien
940	68	6.2	2344	2	Q6QWJ0	Q6qwj0	rabbit hemo
941	68	6.2	2461	2	Q7TN88	Q7tn88	mus musculu
942	68	6.2	8094	2	Q8ILB9	Q8ilb9	plasmodium
943	68	6.2	16223	2	Q8IR22	Q8ir22	drosophila
944	67.5	6.1	136	2	Q6RGL8	Q6rgl8	senna alata
945	67.5	6.1	161	2	Q6ILL1	Q6ill1	drosophila
946	67.5	6.1	193	2	Q60408	Q60408	cavia cutle
947	67.5	6.1	206	2	Q8R479	Q8r479	mus musculu
948	67.5	6.1	207	2	Q8YGX2	Q8ygx2	brucella me
949	67.5	6.1	207	2	Q8G0Z1	Q8g0z1	brucella su
950	67.5	6.1	210	2	Q9FJL8	Q9fjl8	arabidopsis
951	67.5	6.1	220	2	Q37488	Q37488	heliconius
952	67.5	6.1	227	2	Q9GCL6	Q9gcl6	sericinus m
953	67.5	6.1	269	2	Q86FE2	Q86fe2	schistosoma
954	67.5	6.1	270	1	IL1A_PIG	P18430	sus scrofa
955	67.5	6.1	274	2	Q9GKD9	Q9gkd9	bos taurus
956	67.5	6.1	275	2	Q9FZ05	Q9fz05	lycopersico
957	67.5	6.1	278	1	TNF6_RAT	P36940	rattus norv
958	67.5	6.1	280	1	CTX3_MOUSE	Q9d387	mus musculu
959	67.5	6.1	283	2	Q8EUR1	Q8eur1	mycoplasma
960	67.5	6.1	289	1	CYF_MASLA	P83793	mastigoclad
961	67.5	6.1	289	2	Q8KFG5	Q8kfg5	chlorobium
962	67.5	6.1	292	2	Q8LAG0	Q8lag0	arabidopsis
963	67.5	6.1	295	2	Q9QYL6	Q9qyl6	mus musculu
964	67.5	6.1	297	2	Q8HKB4	Q8hkb4	roboastra e
965	67.5	6.1	299	2	Q9EMK9	Q9emk9	amsacta moo
966	67.5	6.1	312	1	LPXK_HELPJ	Q9zmb1	helicobacte
967	67.5	6.1	320	2	Q8GDT5	Q8gdt5	heliobacill
968	67.5	6.1	330	2	Q9ZZQ3	Q9zzq3	cyanidiosch
969	67.5	6.1	341	2	Q7Q1J7	Q7q1j7	anopheles g
970	67.5	6.1	353	2	Q86SV4	Q86sv4	homo sapien
971	67.5	6.1	356	2	Q6K4G2	Q6k4g2	oryza sativ
972	67.5	6.1	361	2	Q8MGX9	Q8mgx9	sus scrofa
973	67.5	6.1	361	2	Q91E16	Q91e16	rice black
974	67.5	6.1	362	2	Q910P9	Q910p9	rice black
975	67.5	6.1	362	2	Q8B4T7	Q8b4t7	rice black
976	67.5	6.1	370	1	C244_HUMAN	Q9bzw8	homo sapien
977	67.5	6.1	378	1	YF69_AQUAE	O67513	aquifex aeo
978	67.5	6.1	387	2	Q17845	Q17845	caenorhabdi
979	67.5	6.1	399	2	Q22079	Q22079	caenorhabdi
980	67.5	6.1	423	2	Q9UYP7	Q9uyp7	pyrococcus

981	67.5	6.1	425	2	Q9BL95	Q9bl95 caenorhabdi	1054	67	6.1	157	2	Q66X97	Q66x97 hesperia co		
982	67.5	6.1	428	2	Q8M968	Q8m968 proboscidea	1055	67	6.1	178	2	Q6CWP0	Q6cwp0 kluyveromyc		
983	67.5	6.1	431	2	Q7RLQ4	Q7rlq4 plasmodium	1056	67	6.1	194	2	Q8LZR9	Q8lzr9 gymnopleuru		
984	67.5	6.1	437	2	Q6FKB2	Q6fkb2 candida gla	1057	67	6.1	215	2	Q9BKZ8	Q9bkz8 caenorhabdi		
985	67.5	6.1	447	2	Q9PHJ1	Q9phj1 xylella fas	1058	67	6.1	220	1	CD28_HUMAN	P10747 homo sapien		
986	67.5	6.1	468	2	Q9RWV3	Q9rwv3 deinococcus	1059	67	6.1	223	2	Q8K837	Q8k837 streptococc		
987	67.5	6.1	472	2	O23699	O23699 arabidopsis	1060	67	6.1	234	2	Q70WG0	Q70wg0 homo sapien		
988	67.5	6.1	475	2	Q8VDD8	Q8vdd8 mus musculu	1061	67	6.1	259	2	Q9NZ43	Q9nz43 homo sapien		
989	67.5	6.1	478	2	Q6AVE3	Q6ave3 oryza sativ	1062	67	6.1	261	1	RFA4_HUMAN	Q13156 homo sapien		
990	67.5	6.1	479	2	Q94KD9	Q94kd9 arabidopsis	1063	67	6.1	290	2	Q8AUN1	Q8aun1 paralabidoc		
991	67.5	6.1	481	2	Q8M970	Q8m970 peltanthera	1064	67	6.1	290	2	Q8AUR6	Q8aur6 yssichromis		
992	67.5	6.1	486	2	O45749	O45749 caenorhabdi	1065	67	6.1	297	2	Q9VFR0	Q9vfr0 drosophila		
993	67.5	6.1	489	2	Q9A762	Q9a762 caulobacter	1066	67	6.1	304	2	Q20981	Q20981 caenorhabdi		
994	67.5	6.1	494	2	Q7ZTK1	Q7ztk1 xenopus lae	1067	67	6.1	304	2	Q9F4C1	Q9f4c1 bacillus me		
995	67.5	6.1	496	2	Q8AZ57	Q8az57 machupo vir	1068	67	6.1	305	2	Q6NB03	Q6nb03 rhodopseudo		
996	67.5	6.1	497	2	Q9LMM7	Q9lmm7 arabidopsis	1069	67	6.1	306	2	Q812U0	Q812u0 bacillus ce		
997	67.5	6.1	500	2	Q7YKM5	Q7ykm5 proboscidea	1070	67	6.1	309	2	O58296	O58296 pyrococcus		
998	67.5	6.1	505	2	Q9Y799	Q9y799 candida par	1071	67	6.1	328	2	Q6M020	Q6m020 methanococc		
999	67.5	6.1	507	2	Q66K78	Q66k78 homo sapien	1072	67	6.1	329	2	Q8W3Y0	Q8w3y0 citrus jamb		
1000	67.5	6.1	508	2	Q9TIS2	Q9tis2 hemimeris s	1073	67	6.1	333	2	Q8CT52	Q8ct52 staphylococ		
1001	67.5	6.1	533	2	Q65JM8	Q65jm8 bacillus li	1074	67	6.1	350	1	CKRB_BOVIN	P35350 bos taurus		
1002	67.5	6.1	539	2	Q8G559	Q8g559 bifidobacte	1075	67	6.1	352	2	Q650L7	Q65017 bacteroides		
1003	67.5	6.1	540	2	Q6NWR2	Q6nwr2 homo sapien	1076	67	6.1	353	2	Q8HX43	Q8hx43 salmo salar		
1004	67.5	6.1	543	2	Q6CBN8	Q6cbn8 yarrowia li	1077	67	6.1	354	2	Q72D61	Q72d61 desulfovibr		
1005	67.5	6.1	561	2	Q8MZ34	Q8mz34 drosophila	1078	67	6.1	355	2	Q8HX44	Q8hx44 salmo salar		
1006	67.5	6.1	570	2	Q6GJX3	Q6gjx3 staphylococ	1079	67	6.1	357	2	Q76DX8	Q76dx8 plecoglossu		
1007	67.5	6.1	589	2	Q6P4C8	Q6p4c8 homo sapien	1080	67	6.1	359	2	Q9W771	Q9w771 columba liv		
1008	67.5	6.1	589	2	Q7PB25	Q7pb25 rickettsia	1081	67	6.1	364	1	OPSR_HUMAN	P04000 homo sapien		
1009	67.5	6.1	589	2	Q92IY4	Q92iy4 rickettsia	1082	67	6.1	366	2	Q97N34	Q97n34 clostridium		
1010	67.5	6.1	607	2	Q8K2I7	Q8k2i7 mus musculu	1083	67	6.1	378	2	Q95I95	Q95i95 stizostedio		
1011	67.5	6.1	608	1	YD93_METJA	Q58788 methanococc	1084	67	6.1	379	2	Q6BPL6	Q6bpl6 debaryomyce		
1012	67.5	6.1	612	1	LEM2_MOUSE	Q00690 mus musculu	1085	67	6.1	386	2	Q63EG1	Q63eg1 bacillus ce		
1013	67.5	6.1	622	2	Q91570	Q91570 xenopus lae	1086	67	6.1	400	2	Q8C5E4	Q8c5e4 mus musculu		
1014	67.5	6.1	656	1	SL54_MOUSE	Q9et37 mus musculu	1087	67	6.1	406	2	Q9QAT4	Q9qat4 african swi		
1015	67.5	6.1	657	2	O93127	O93127 spodoptera	1088	67	6.1	413	1	CVAA_ECOLI	P22519 escherichia		
1016	67.5	6.1	666	2	Q9XED4	Q9xed4 phaseolus v	1089	67	6.1	413	2	Q6KDB4	Q6kdb4 escherichia		
1017	67.5	6.1	669	2	Q6ARA9	Q6ara9 desulfotale	1090	67	6.1	413	2	Q9RPH4	Q9rph4 mycobacteri		
1018	67.5	6.1	689	2	Q74AA9	Q74aa9 geobacter s	1091	67	6.1	415	2	Q73AC4	Q73ac4 bacillus ce		
1019	67.5	6.1	724	2	Q96GR2	Q96gr2 homo sapien	1092	67	6.1	418	2	Q766V2	Q766v2 gallus gall		
1020	67.5	6.1	724	2	Q9HC26	Q9hc26 homo sapien	1093	67	6.1	424	1	MCHE_ECOLI	Q9exn6 escherichia		
1021	67.5	6.1	729	2	Q76N27	Q76n27 homo sapien	1094	67	6.1	424	2	Q83Z98	Q83z98 escherichia		
1022	67.5	6.1	730	2	Q8WX65	Q8wx65 homo sapien	1095	67	6.1	424	2	Q83ZA5	Q83za5 escherichia		
1023	67.5	6.1	755	2	Q9LWP2	Q9lwp2 oryza sativ	1096	67	6.1	424	2	Q841V2	Q841v2 escherichia		
1024	67.5	6.1	790	2	Q91838	Q91838 xenopus lae	1097	67	6.1	424	2	Q8FIX7	Q8fix7 escherichia		
1025	67.5	6.1	827	2	Q80WQ6	Q80wq6 mus musculu	1098	67	6.1	437	2	Q7M8Y7	Q7m8y7 wolinella s		
1026	67.5	6.1	827	2	Q8BJ70	Q8bj70 mus musculu	1099	67	6.1	445	2	Q8HVX4	Q8hvx4 clerodendru		
1027	67.5	6.1	854	2	Q6MYT3	Q6myt3 aspergillus	1100	67	6.1	446	2	Q66S01	Q66s01 oikopleura		
1028	67.5	6.1	915	2	Q7S8E9	Q7s8e9 neurospora	1101	67	6.1	447	2	Q8HVX3	Q8hvx3 clerodendru		
1029	67.5	6.1	991	2	Q7SEQ2	Q7seq2 neurospora	1102	67	6.1	447	2	Q64Y00	Q64y00 bacteroides		
1030	67.5	6.1	1035	2	Q9M7J0	Q9m7j0 populus tre	1103	67	6.1	452	2	Q83R24	Q83r24 shigella fl		
1031	67.5	6.1	1048	2	Q92T03	Q92t03 rhizobium m	1104	67	6.1	467	2	Q8ZE93	Q8ze93 yersinia pe		
1032	67.5	6.1	1049	2	Q9AUJ8	Q9auj8 oryza sativ	1105	67	6.1	477	2	Q8CYN0	Q8cyn0 streptococc		
1033	67.5	6.1	1053	1	ITA5_MOUSE	P11688 mus musculu	1106	67	6.1	477	2	Q8D0H7	Q8d0h7 yersinia pe		
1034	67.5	6.1	1053	2	Q80YP5	Q80yp5 mus musculu	1107	67	6.1	479	2	Q98S64	Q98s64 guillardia		
1035	67.5	6.1	1078	2	Q7Y010	Q7y010 oryza sativ	1108	67	6.1	491	2	Q6C1G6	Q6c1g6 yarrowia li		
1036	67.5	6.1	1222	2	Q86HL6	Q86hl6 dictyosteli	1109	67	6.1	496	2	Q7NA26	Q7na26 photorhabdu		
1037	67.5	6.1	1222	2	Q86SA4	Q86sa4 dictyosteli	1110	67	6.1	504	2	Q8SN35	Q8sn35 diplopanax		
1038	67.5	6.1	1313	2	Q723Y0	Q723y0 listeria mo	1111	67	6.1	506	2	O25480	O25480 helicobacte		
1039	67.5	6.1	1375	2	Q8ML47	Q8ml47 drosophila	1112	67	6.1	509	2	Q995C5	Q995c5 pirital vir		
1040	67.5	6.1	1375	2	Q94537	Q94537 drosophila	1113	67	6.1	512	1	FLO1_RAT	Q62866 rattus norv		
1041	67.5	6.1	1523	2	Q7RS28	Q7rs28 plasmodium	1114	67	6.1	512	2	Q9QUM8	Q9qum8 rattus norv		
1042	67.5	6.1	1526	2	Q94538	Q94538 drosophila	1115	67	6.1	518	2	Q8RC50	Q8rc50 thermoanaer		
1043	67.5	6.1	1526	2	Q9V6D5	Q9v6d5 drosophila	1116	67	6.1	553	2	Q8MPX9	Q8mpx9 caenorhabdi		
1044	67.5	6.1	1894	2	Q64487	Q64487 mus musculu	1117	67	6.1	558	2	Q22938	Q22938 caenorhabdi		
1045	67.5	6.1	1912	1	PTPD_HUMAN	P23468 homo sapien	1118	67	6.1	566	2	Q8PL71	Q8pl71 xanthomonas		
1046	67.5	6.1	2066	2	P89920	P89920 oat blue dw	1119	67	6.1	586	2	Q69JG2	Q69jg2 oryza sativ		
1047	67.5	6.1	2720	2	Q8IPG4	Q8ipg4 drosophila	1120	67	6.1	591	2	Q22271	Q22271 caenorhabdi		
1048	67.5	6.1	2771	2	Q9VLS3	Q9vls3 drosophila	1121	67	6.1	605	2	Q6GNL9	Q6gnl9 xenopus lae		
1049	67.5	6.1	3665	2	Q7UQ60	Q7uq60 rhodopirell	1122	67	6.1	648	2	Q7KWN1	Q7kwn1 dictyosteli		
1050	67.5	6.1	4834	2	O95714	O95714 homo sapien	1123	67	6.1	650	2	Q9SKL8	Q9skl8 arabidopsis		
1051	67	6.1	43	2	P79464	P79464 bos taurus	1124	67	6.1	673	2	Q9VW10	Q9vw10 drosophila		
1052	67	6.1	95	1	FXY6_HUMAN	Q9h0q3 homo sapien	1125	67	6.1	701	1	HRPH_PSESY	Q01723 pseudomonas		
1053	67	6.1	120	2	Q6UW52	Q6uw52 homo sapien	1126	67	6.1	705	2	O85969	O85969 sphingomona		

1127	67	6.1	714	2	Q6ZPE6	Q6zpe6 mus musculu
1128	67	6.1	720	2	Q40902	Q40902 petunia int
1129	67	6.1	730	2	Q8D9P1	Q8d9p1 vibrio vuln
1130	67	6.1	782	2	Q18654	Q18654 caenorhabdi
1131	67	6.1	790	2	Q94GL4	Q94gl4 oryza sativ
1132	67	6.1	803	2	Q6P9F7	Q6p9f7 homo sapien
1133	67	6.1	829	1	CADG_HUMAN	O75309 homo sapien
1134	67	6.1	836	2	Q9V3Q9	Q9v3q9 drosophila
1135	67	6.1	840	2	Q9BML7	Q9bml7 drosophila
1136	67	6.1	842	2	Q83XL3	Q83xl3 legionella
1137	67	6.1	868	2	Q9SDN6	Q9sdn6 nicotiana t
1138	67	6.1	906	1	CADO_XENLA	P33147 xenopus lae
1139	67	6.1	956	1	GLK4_RAT	Q01812 rattus norv
1140	67	6.1	1009	2	Q9U458	Q9u458 drosophila
1141	67	6.1	1017	2	Q90X34	Q90x34 brachydanio
1142	67	6.1	1017	2	Q9DGL5	Q9dgl5 brachydanio
1143	67	6.1	1023	1	A1A1_BUFMA	P30714 bufo marinu
1144	67	6.1	1023	1	A1A1_OREMO	Q9yh26 oreochromis
1145	67	6.1	1024	2	Q90X33	Q90x33 brachydanio
1146	67	6.1	1024	2	Q9DEU0	Q9deu0 brachydanio
1147	67	6.1	1032	1	A1A4_MOUSE	Q9wv27 mus musculu
1148	67	6.1	1034	2	Q9TUN4	Q9tun4 oryctolagus
1149	67	6.1	1117	2	Q6P1C6	Q6p1c6 mus musculu
1150	67	6.1	1127	2	Q7R5V0	Q7r5v0 giardia lam
1151	67	6.1	1199	2	Q8D7L5	Q8d7l5 vibrio vuln
1152	67	6.1	1348	2	Q25199	Q25199 hydra atten
1153	67	6.1	1361	1	RSE1_YEAST	Q04693 saccharomyc
1154	67	6.1	1382	1	MET_RAT	P97523 rattus norv
1155	67	6.1	1529	2	Q67VX5	Q67vx5 oryza sativ
1156	67	6.1	1556	2	Q9W159	Q9w159 drosophila
1157	67	6.1	1593	2	Q8T6H1	Q8t6h1 dictyosteli
1158	67	6.1	2829	2	Q6IVD6	Q6ivd6 strongyloce
1159	66.5	6.0	108	2	Q6S7D7	Q6s7d7 sus scrofa
1160	66.5	6.0	135	2	Q9KBZ2	Q9kbz2 bacillus ha
1161	66.5	6.0	155	2	Q64F76	Q64f76 lactococcus
1162	66.5	6.0	155	2	Q64F77	Q64f77 lactococcus
1163	66.5	6.0	155	2	Q64F79	Q64f79 lactococcus
1164	66.5	6.0	155	2	Q64F83	Q64f83 lactococcus
1165	66.5	6.0	203	2	Q6PYV4	Q6pyv4 schistosoma
1166	66.5	6.0	228	2	Q8SGU3	Q8sgu3 drosophila
1167	66.5	6.0	231	1	HGXR_PLAFK	P07833 plasmodium
1168	66.5	6.0	268	2	Q9EP57	Q9ep57 mus musculu
1169	66.5	6.0	268	2	Q9JIQ1	Q9jiq1 mus musculu
1170	66.5	6.0	270	2	Q6SWS0	Q6sws0 human cytom
1171	66.5	6.0	271	2	Q6DGI9	Q6dgi9 brachydanio
1172	66.5	6.0	273	2	Q9JMA4	Q9jma4 mus musculu
1173	66.5	6.0	274	2	Q8BJS9	Q8bjs9 mus musculu
1174	66.5	6.0	281	2	Q9JIQ2	Q9jiq2 mus musculu
1175	66.5	6.0	285	2	Q87UH6	Q87uh6 pseudomonas
1176	66.5	6.0	289	2	Q6GP29	Q6gp29 xenopus lae
1177	66.5	6.0	295	2	Q9Z2H8	Q9z2h8 mus musculu
1178	66.5	6.0	307	2	Q645U6	Q645u6 pongo pygma
1179	66.5	6.0	309	2	Q646A0	Q646a0 gorilla gor
1180	66.5	6.0	318	2	Q62EV0	Q62ev0 burkholderi
1181	66.5	6.0	318	2	Q63YD3	Q63yd3 burkholderi
1182	66.5	6.0	325	2	O02838	O02838 sus scrofa
1183	66.5	6.0	356	2	Q8HX66	Q8hx66 sus scrofa
1184	66.5	6.0	361	2	Q8MGQ5	Q8mgq5 sus scrofa
1185	66.5	6.0	361	2	Q8MHT8	Q8mht8 sus scrofa
1186	66.5	6.0	364	2	O19245	O19245 sus scrofa
1187	66.5	6.0	364	2	Q8MHU4	Q8mhu4 sus scrofa
1188	66.5	6.0	364	2	Q31068	Q31068 sus scrofa
1189	66.5	6.0	364	2	Q8BV78	Q8bv78 mus musculu
1190	66.5	6.0	366	2	Q31069	Q31069 sus scrofa
1191	66.5	6.0	369	2	Q84EK9	Q84ek9 shewanella
1192	66.5	6.0	378	2	Q8I642	Q8i642 plasmodium
1193	66.5	6.0	379	2	Q8PWN2	Q8pwn2 methanosarc
1194	66.5	6.0	390	2	Q7PQJ8	Q7pqj8 anopheles g
1195	66.5	6.0	393	1	PKR1_HUMAN	Q8tcw9 homo sapien
1196	66.5	6.0	395	2	Q877W4	Q877w4 streptococc
1197	66.5	6.0	400	2	Q54867	Q54867 streptococc
1198	66.5	6.0	403	2	Q7NFQ1	Q7nfq1 gloeobacter
1199	66.5	6.0	404	2	Q54866	Q54866 streptococc
1200	66.5	6.0	415	2	Q8A7I8	Q8a7i8 bacteroides
1201	66.5	6.0	419	1	HASA_STRPY	Q54865 streptococc
1202	66.5	6.0	419	2	Q8K5G6	Q8k5g6 streptococc
1203	66.5	6.0	419	2	Q8NKX1	Q8nkx1 streptococc
1204	66.5	6.0	422	2	Q6QAN7	Q6qan7 carassius a
1205	66.5	6.0	423	2	Q8N2D4	Q8n2d4 homo sapien
1206	66.5	6.0	425	2	Q18923	Q18923 caenorhabdi
1207	66.5	6.0	439	2	Q9H2V8	Q9h2v8 homo sapien
1208	66.5	6.0	439	2	Q72R28	Q72r28 leptospira
1209	66.5	6.0	441	2	Q816E9	Q816e9 bacillus ce
1210	66.5	6.0	442	2	Q9BY67	Q9by67 homo sapien
1211	66.5	6.0	443	2	Q6VLX3	Q6vlx3 mus musculu
1212	66.5	6.0	444	1	OX2R_HUMAN	O43614 homo sapien
1213	66.5	6.0	444	2	Q632F1	Q632f1 bacillus ce
1214	66.5	6.0	444	2	Q72YH1	Q72yh1 bacillus ce
1215	66.5	6.0	444	2	Q81K62	Q81k62 bacillus an
1216	66.5	6.0	444	2	Q6HBZ4	Q6hbz4 bacillus th
1217	66.5	6.0	445	2	Q8K3T6	Q8k3t6 mus musculu
1218	66.5	6.0	445	2	Q8R4L1	Q8r4l1 mus musculu
1219	66.5	6.0	460	1	OX2R_MOUSE	P58308 mus musculu
1220	66.5	6.0	460	1	OX2R_RAT	P56719 rattus norv
1221	66.5	6.0	468	2	Q9NZL2	Q9nzl2 homo sapien
1222	66.5	6.0	482	1	MURE_AQUAE	O67631 aquifex aeo
1223	66.5	6.0	485	2	Q88SB5	Q88sb5 lactobacill
1224	66.5	6.0	489	1	YHIP_ECOLI	P36837 escherichia
1225	66.5	6.0	489	2	Q8FCL2	Q8fcl2 escherichia
1226	66.5	6.0	489	2	Q8X5Q8	Q8x5q8 escherichia
1227	66.5	6.0	496	2	Q6IUF7	Q6iuf7 machupo vir
1228	66.5	6.0	496	2	Q6IVT5	Q6ivt5 machupo vir
1229	66.5	6.0	496	2	Q6PXP4	Q6pxp4 machupo vir
1230	66.5	6.0	510	2	Q9SJ08	Q9sj08 arabidopsis
1231	66.5	6.0	512	2	Q6ZFB3	Q6zfb3 oryza sativ
1232	66.5	6.0	518	1	BAE2_HUMAN	Q9y5z0 homo sapien
1233	66.5	6.0	518	2	Q85IK9	Q85ik9 beta vulgar
1234	66.5	6.0	523	2	Q6BYQ4	Q6byq4 debaryomyce
1235	66.5	6.0	529	2	Q7NNH4	Q7nnh4 gloeobacter
1236	66.5	6.0	534	2	Q8QZV1	Q8qzv1 rattus norv
1237	66.5	6.0	536	2	Q8KG54	Q8kg54 chlorobium
1238	66.5	6.0	539	2	Q8CFW3	Q8cfw3 mus musculu
1239	66.5	6.0	558	2	Q8T4C6	Q8t4c6 drosophila
1240	66.5	6.0	568	2	Q6KYX3	Q6kyx3 picrophilus
1241	66.5	6.0	571	2	O57604	O57604 gallus gall
1242	66.5	6.0	600	2	Q86BE1	Q86be1 drosophila
1243	66.5	6.0	603	2	Q7KRC4	Q7krc4 drosophila
1244	66.5	6.0	606	2	Q8DMG6	Q8dmg6 synechococc
1245	66.5	6.0	661	2	Q8F4Q8	Q8f4q8 leptospira
1246	66.5	6.0	712	2	Q7X660	Q7x660 oryza sativ
1247	66.5	6.0	721	2	Q6DDN6	Q6ddn6 xenopus lae
1248	66.5	6.0	729	2	Q8LBQ6	Q8lbq6 arabidopsis
1249	66.5	6.0	733	2	Q9FKQ8	Q9fkq8 arabidopsis
1250	66.5	6.0	757	2	Q82L71	Q82l71 streptomyce
1251	66.5	6.0	777	2	Q6BG55	Q6bg55 paramecium
1252	66.5	6.0	830	1	HMT1_SCHPO	Q02592 schizosacch
1253	66.5	6.0	830	2	Q665G7	Q665g7 yersinia ps
1254	66.5	6.0	830	2	Q6QDZ2	Q6qdz2 yersinia ps
1255	66.5	6.0	837	2	Q6FZA3	Q6fza3 bartonella
1256	66.5	6.0	964	2	Q82IQ4	Q82iq4 streptomyce
1257	66.5	6.0	973	2	Q7Q438	Q7q438 anopheles g
1258	66.5	6.0	1030	2	Q17443	Q17443 caenorhabdi
1259	66.5	6.0	1081	2	O76809	O76809 hydra atten
1260	66.5	6.0	1088	2	Q9XX01	Q9xx01 caenorhabdi
1261	66.5	6.0	1119	2	Q86G88	Q86g88 pseudoplusi
1262	66.5	6.0	1136	2	Q6EUT8	Q6eut8 caenorhabdi
1263	66.5	6.0	1200	2	Q6CJF8	Q6cjf8 kluyveromyc
1264	66.5	6.0	1210	2	Q7YTI9	Q7yti9 caenorhabdi
1265	66.5	6.0	1349	2	Q92EV6	Q92ev6 listeria in
1266	66.5	6.0	1406	2	O01777	O01777 caenorhabdi
1267	66.5	6.0	1522	2	Q756Z0	Q756z0 ashbya goss
1268	66.5	6.0	1542	2	Q7KVP4	Q7kvp4 drosophila
1269	66.5	6.0	1546	2	Q86BS7	Q86bs7 drosophila
1270	66.5	6.0	1629	2	Q9W2H8	Q9w2h8 drosophila
1271	66.5	6.0	1687	2	Q7Q1M9	Q7q1m9 anopheles g
1272	66.5	6.0	1697	2	Q7RTE2	Q7rte2 plasmodium

1273	66.5	6.0	1729	2	Q7SCY4	Q7scy4	neurospora
1274	66.5	6.0	1770	1	RI15_YEAST	P43565	saccharomyc
1275	66.5	6.0	1821	2	Q9R0C4	Q9r0c4	mus musculu
1276	66.5	6.0	2013	2	Q8VHZ8	Q8vhz8	rattus norv
1277	66.5	6.0	2013	2	Q9ERC8	Q9erc8	mus musculu
1278	66.5	6.0	2231	2	Q75EK8	Q75ek8	ashbya goss
1279	66.5	6.0	2325	2	Q9N3X8	Q9n3x8	caenorhabdi
1280	66.5	6.0	2799	1	G112_HUMAN	Q8izf6	homo sapien
1281	66.5	6.0	3069	2	Q702P4	Q702p4	homo sapien
1282	66.5	6.0	3135	2	Q709D0	Q709d0	homo sapien
1283	66.5	6.0	3174	1	V13A_HUMAN	Q96rl7	homo sapien
1284	66.5	6.0	4803	2	Q84BC7	Q84bc7	nostoc sp.
1285	66	6.0	128	2	Q6NDN8	Q6ndn8	rhodopseudo
1286	66	6.0	167	2	Q82UD2	Q82ud2	nitrosomona
1287	66	6.0	179	2	Q9TXX1	Q9txx1	caenorhabdi
1288	66	6.0	193	1	Y319_MYCPN	P75329	mycoplasma
1289	66	6.0	206	2	Q72MU3	Q72mu3	leptospira
1290	66	6.0	223	2	Q8P1L8	Q8p1l8	streptococc
1291	66	6.0	223	2	Q9A0K2	Q9a0k2	streptococc
1292	66	6.0	226	1	RR46_SCHPO	O42894	schizosacch
1293	66	6.0	247	2	Q9KKI3	Q9kki3	yersinia en
1294	66	6.0	248	2	Q96J10	Q96j10	homo sapien
1295	66	6.0	251	2	Q7P0X7	Q7p0x7	chromobacte
1296	66	6.0	252	1	KSGA_MYCPU	Q98rj3	mycoplasma
1297	66	6.0	252	2	Q68X29	Q68x29	rickettsia
1298	66	6.0	253	2	Q62323	Q62323	mus musculu
1299	66	6.0	257	2	Q7NCX6	Q7ncx6	gloeobacter
1300	66	6.0	260	2	Q9XWS8	Q9xws8	caenorhabdi
1301	66	6.0	265	2	Q8XX82	Q8xx82	ralstonia s
1302	66	6.0	267	2	O28582	O28582	archaeoglob
1303	66	6.0	268	2	Q8NQ71	Q8nq71	corynebacte
1304	66	6.0	268	2	Q8G877	Q8g877	bifidobacte
1305	66	6.0	275	2	Q9FI02	Q9fi02	arabidopsis
1306	66	6.0	277	2	Q7WNL8	Q7wnl8	bordetella
1307	66	6.0	284	2	Q9PJ62	Q9pj62	campylobact
1308	66	6.0	298	2	Q8KYN2	Q8kyn2	bacillus an
1309	66	6.0	298	2	Q6EZR6	Q6ezr6	bacillus an
1310	66	6.0	299	2	Q73S22	Q73s22	mycobacteri
1311	66	6.0	307	2	Q6I1Y2	Q6i1y2	bacillus an
1312	66	6.0	308	2	Q8UIT4	Q8uit4	agrobacteri
1313	66	6.0	317	2	Q9D3N6	Q9d3n6	mus musculu
1314	66	6.0	327	2	Q7TRQ9	Q7trq9	mus musculu
1315	66	6.0	328	2	Q7D1Y6	Q7d1y6	agrobacteri
1316	66	6.0	328	2	Q7VA71	Q7va71	prochloroco
1317	66	6.0	328	2	Q9WI11	Q9wi11	bovine herp
1318	66	6.0	331	2	Q704Z8	Q704z8	rubus idaeu
1319	66	6.0	332	2	Q6DVN2	Q6dvn2	triops long
1320	66	6.0	334	2	Q6ZR97	Q6zr97	homo sapien
1321	66	6.0	338	2	Q6HIG1	Q6hig1	bacillus th
1322	66	6.0	340	2	Q9BHL2	Q9bhl2	caenorhabdi
1323	66	6.0	341	2	O87531	O87531	streptococc
1324	66	6.0	341	2	Q7CMM6	Q7cmm6	streptococc
1325	66	6.0	343	2	Q7QCT9	Q7qct9	anopheles g
1326	66	6.0	345	2	Q7P3R6	Q7p3r6	fusobacteri
1327	66	6.0	357	1	OPSR_ASTFA	P22332	astyanax fa
1328	66	6.0	361	2	Q94IA7	Q94ia7	nicotiana t
1329	66	6.0	362	2	Q8IJV1	Q8ijv1	plasmodium
1330	66	6.0	362	2	Q95IT0	Q95it0	trichosurus
1331	66	6.0	364	2	Q9XSX3	Q9xsx3	macaca fasc
1332	66	6.0	365	2	Q20731	Q20731	caenorhabdi
1333	66	6.0	365	2	Q9YI52	Q9yi52	ambystoma t
1334	66	6.0	368	2	Q64RH0	Q64rh0	bacteroides
1335	66	6.0	384	1	PKR2_BOVIN	Q8spn1	bos taurus
1336	66	6.0	384	1	PKR2_HUMAN	Q8nfj6	homo sapien
1337	66	6.0	393	1	PKR1_BOVIN	Q8spn2	bos taurus
1338	66	6.0	411	2	Q87IP7	Q87ip7	vibrio para
1339	66	6.0	413	2	Q8XFG0	Q8xfg0	salmonella
1340	66	6.0	413	2	Q7CP73	Q7cp73	salmonella
1341	66	6.0	445	2	Q9NJM2	Q9njm2	endeis laev
1342	66	6.0	450	2	Q95BP9	Q95bp9	trichopilia
1343	66	6.0	452	2	Q8ZVR8	Q8zvr8	pyrobaculum
1344	66	6.0	453	2	Q9PJY6	Q9pjy6	chlamydia m
1345	66	6.0	477	2	Q97Q66	Q97q66	streptococc
1346	66	6.0	480	2	O65483	O65483	arabidopsis
1347	66	6.0	482	2	Q66AC0	Q66ac0	yersinia ps
1348	66	6.0	495	2	Q6CC13	Q6cc13	yarrowia li
1349	66	6.0	503	1	VGLY_PIARV	P03540	pichinde ar
1350	66	6.0	508	2	O11997	O11997	pichinde ar
1351	66	6.0	508	2	O11998	O11998	pichinde ar
1352	66	6.0	509	2	Q94AR8	Q94ar8	arabidopsis
1353	66	6.0	509	2	Q9T0L4	Q9t0l4	arabidopsis
1354	66	6.0	509	2	O11999	O11999	pichinde ar
1355	66	6.0	526	1	CEA1_HUMAN	P13688	homo sapien
1356	66	6.0	526	2	Q701P1	Q701p1	fusarium pr
1357	66	6.0	529	2	Q8WUV6	Q8wuv6	homo sapien
1358	66	6.0	532	2	Q8EQY3	Q8eqy3	oceanobacil
1359	66	6.0	532	2	Q8EZU8	Q8ezu8	leptospira
1360	66	6.0	539	2	Q9M811	Q9m811	arabidopsis
1361	66	6.0	572	2	P71187	P71187	enterobacte
1362	66	6.0	573	2	Q23530	Q23530	caenorhabdi
1363	66	6.0	605	2	Q6UVY4	Q6uvy4	homo sapien
1364	66	6.0	605	2	Q9NZ53	Q9nz53	homo sapien
1365	66	6.0	620	2	Q9NEG8	Q9neg8	leishmania
1366	66	6.0	623	2	O23521	O23521	arabidopsis
1367	66	6.0	631	2	P71143	P71143	clostridium
1368	66	6.0	652	2	Q7VN07	Q7vn07	haemophilus
1369	66	6.0	653	1	LRR4_HUMAN	Q9hbw1	homo sapien
1370	66	6.0	654	1	PSTA_MYCGE	P47651	mycoplasma
1371	66	6.0	698	1	ALT_BPT2	Q38424	bacteriopha
1372	66	6.0	705	2	Q9UIX2	Q9uix2	homo sapien
1373	66	6.0	710	2	Q9M0H1	Q9m0h1	arabidopsis
1374	66	6.0	718	2	Q38887	Q38887	arabidopsis
1375	66	6.0	726	2	Q6FXV8	Q6fxv8	candida gla
1376	66	6.0	730	2	Q7MKP2	Q7mkp2	vibrio vuln
1377	66	6.0	735	2	O64505	O64505	arabidopsis
1378	66	6.0	748	2	Q6DRC2	Q6drc2	brachydanio
1379	66	6.0	782	2	Q9H9V8	Q9h9v8	homo sapien
1380	66	6.0	782	2	Q8X6V4	Q8x6v4	escherichia
1381	66	6.0	782	2	Q9Z1H6	Q9z1h6	mus musculu
1382	66	6.0	782	2	Q8VDF2	Q8vdf2	mus musculu
1383	66	6.0	784	2	Q7XL86	Q7xl86	oryza sativ
1384	66	6.0	786	2	Q73W24	Q73w24	mycobacteri
1385	66	6.0	798	2	Q9GLP0	Q9glp0	sus scrofa
1386	66	6.0	798	2	Q6P4X1	Q6p4x1	xenopus tro
1387	66	6.0	820	2	Q6D0P8	Q6d0p8	erwinia car
1388	66	6.0	830	2	Q8IWA0	Q8iwa0	homo sapien
1389	66	6.0	835	2	Q6DCP0	Q6dcp0	xenopus lae
1390	66	6.0	901	2	Q8GDJ9	Q8gdj9	photorhabdu
1391	66	6.0	946	2	Q9LT96	Q9lt96	arabidopsis
1392	66	6.0	956	1	GLK4_HUMAN	Q16099	homo sapien
1393	66	6.0	1076	1	RPOB_ASTLO	P27059	astasia lon
1394	66	6.0	1115	1	ITA3_DROME	O44386	drosophila
1395	66	6.0	1117	2	Q89ZX4	Q89zx4	bacteroides
1396	66	6.0	1155	2	Q7QF51	Q7qf51	anopheles g
1397	66	6.0	1166	2	Q9LAS7	Q9las7	agrobacteri
1398	66	6.0	1330	2	Q6CHC3	Q6chc3	yarrowia li
1399	66	6.0	1372	2	Q6FMR4	Q6fmr4	candida gla
1400	66	6.0	1401	2	Q7KWQ9	Q7kwq9	dictyosteli
1401	66	6.0	1536	1	SIN3_YEAST	P22579	saccharomyc
1402	66	6.0	1726	2	Q6XHB2	Q6xhb2	dictyosteli
1403	66	6.0	2089	2	Q9M067	Q9m067	arabidopsis
1404	66	6.0	2160	2	O17709	O17709	caenorhabdi
1405	66	6.0	2322	2	Q9DYD4	Q9dyd4	rabbit hemo
1406	66	6.0	3207	2	Q8MWQ3	Q8mwq3	plasmodium
1407	66	6.0	3283	2	Q7RP14	Q7rp14	plasmodium
1408	66	6.0	3738	2	O65645	O65645	arabidopsis
1409	65.5	5.9	82	2	Q8R4P3	Q8r4p3	mus musculu
1410	65.5	5.9	110	2	Q7VBU8	Q7vbu8	prochloroco
1411	65.5	5.9	145	2	Q9UL20	Q9ul20	homo sapien
1412	65.5	5.9	149	1	YB29_MYCPN	P75346	mycoplasma
1413	65.5	5.9	155	2	Q860J1	Q860j1	giraffa cam
1414	65.5	5.9	155	2	Q64F78	Q64f78	lactococcus
1415	65.5	5.9	157	2	Q7Z549	Q7z549	homo sapien
1416	65.5	5.9	166	2	Q7Z548	Q7z548	homo sapien
1417	65.5	5.9	192	2	Q8ZN01	Q8zn01	salmonella
1418	65.5	5.9	215	1	RAN_BRUMA	P38542	brugia mala

1419	65.5	5.9	216	2	Q8I2L5	Q8i2l5 plasmodium
1420	65.5	5.9	218	2	Q7NHE5	Q7nhe5 gloeobacter
1421	65.5	5.9	220	2	O66176	O66176 agrobacteri
1422	65.5	5.9	220	2	Q7D2P8	Q7d2p8 agrobacteri
1423	65.5	5.9	227	2	Q13513	Q13513 homo sapien
1424	65.5	5.9	229	2	O63549	O63549 drosophila
1425	65.5	5.9	231	2	Q8IJS1	Q8ijs1 plasmodium
1426	65.5	5.9	243	2	Q9UEL4	Q9uel4 homo sapien
1427	65.5	5.9	269	2	O95297	O95297 homo sapien
1428	65.5	5.9	271	2	Q9LR66	Q9lr66 arabidopsis
1429	65.5	5.9	273	2	Q6DUV0	Q6duv0 mus musculu
1430	65.5	5.9	279	2	Q7TST0	Q7tst0 mus musculu
1431	65.5	5.9	285	1	FCG2_RAT	Q63203 rattus norv
1432	65.5	5.9	292	2	Q9FY94	Q9fy94 arabidopsis
1433	65.5	5.9	294	2	Q9MZV0	Q9mzv0 canis famil
1434	65.5	5.9	298	2	Q8K319	Q8k319 mus musculu
1435	65.5	5.9	298	2	Q804R4	Q804r4 brachydanio
1436	65.5	5.9	309	2	Q645T5	Q645t5 macaca mula
1437	65.5	5.9	309	2	Q646G1	Q646g1 papio hamad
1438	65.5	5.9	311	1	OLF1_CANFA	Q95154 canis famil
1439	65.5	5.9	315	2	Q9U3C7	Q9u3c7 caenorhabdi
1440	65.5	5.9	330	2	Q8MRA7	Q8mra7 drosophila
1441	65.5	5.9	330	2	Q9VP58	Q9vp58 drosophila
1442	65.5	5.9	331	2	Q9XV83	Q9xv83 caenorhabdi
1443	65.5	5.9	338	2	Q7NJ10	Q7nj10 gloeobacter
1444	65.5	5.9	344	2	Q6P6J9	Q6p6j9 mus musculu
1445	65.5	5.9	348	2	Q94T19	Q94t19 caelorinchu
1446	65.5	5.9	349	2	Q6LP34	Q6lp34 photobacter
1447	65.5	5.9	352	2	Q8MHT1	Q8mht1 sus scrofa
1448	65.5	5.9	352	2	Q8SPA6	Q8spa6 sus scrofa
1449	65.5	5.9	352	2	Q8SPA7	Q8spa7 sus scrofa
1450	65.5	5.9	352	2	Q8SPB0	Q8spb0 sus scrofa
1451	65.5	5.9	359	2	Q7XQP4	Q7xqp4 oryza sativ
1452	65.5	5.9	360	2	Q8SPB8	Q8spb8 sus scrofa
1453	65.5	5.9	361	2	O19075	O19075 sus scrofa
1454	65.5	5.9	361	2	Q8HX69	Q8hx69 sus scrofa
1455	65.5	5.9	361	2	Q8MHT7	Q8mht7 sus scrofa
1456	65.5	5.9	361	2	Q8MHT9	Q8mht9 sus scrofa
1457	65.5	5.9	361	2	Q8SPC1	Q8spc1 sus scrofa
1458	65.5	5.9	361	2	Q860V1	Q860v1 sus scrofa
1459	65.5	5.9	361	2	Q860V2	Q860v2 sus scrofa
1460	65.5	5.9	363	1	LEU3_SALTI	Q8z9i1 salmonella
1461	65.5	5.9	363	2	Q7KTW4	Q7ktw4 drosophila
1462	65.5	5.9	364	2	O19243	O19243 sus scrofa
1463	65.5	5.9	364	2	Q8SPC2	Q8spc2 sus scrofa
1464	65.5	5.9	364	2	Q860U6	Q860u6 sus scrofa
1465	65.5	5.9	364	2	Q860U9	Q860u9 sus scrofa
1466	65.5	5.9	364	2	O41525	O41525 canine herp
1467	65.5	5.9	367	2	Q9GIW7	Q9giw7 ictalurus p
1468	65.5	5.9	369	2	Q8BV80	Q8bv80 mus musculu
1469	65.5	5.9	372	2	Q90Y50	Q90y50 brachydanio
1470	65.5	5.9	374	2	Q7VSX4	Q7vsx4 bordetella
1471	65.5	5.9	374	2	Q7W2T8	Q7w2t8 bordetella
1472	65.5	5.9	374	2	Q7WDT6	Q7wdt6 bordetella
1473	65.5	5.9	383	2	Q7T1C0	Q7t1c0 brachydanio
1474	65.5	5.9	403	2	Q6NZV3	Q6nzv3 brachydanio
1475	65.5	5.9	414	2	Q7RPC9	Q7rpc9 plasmodium
1476	65.5	5.9	417	2	P72520	P72520 streptococc
1477	65.5	5.9	417	2	Q8A7J2	Q8a7j2 bacteroides
1478	65.5	5.9	435	2	O45851	O45851 caenorhabdi
1479	65.5	5.9	443	2	Q8HVX8	Q8hvx8 avicennia m
1480	65.5	5.9	443	2	Q71KW2	Q71kw2 avicennia m
1481	65.5	5.9	444	1	OX2R_CANFA	Q9tup7 canis famil
1482	65.5	5.9	450	2	O04601	O04601 arabidopsis
1483	65.5	5.9	452	2	Q7V2G4	Q7v2g4 prochloroco
1484	65.5	5.9	476	1	YG32_YEAST	P53270 saccharomyc
1485	65.5	5.9	479	2	Q8AYW1	Q8ayw1 guanarito v
1486	65.5	5.9	482	1	VGLY_TACV7	P31842 tacaribe vi
1487	65.5	5.9	485	2	O65475	O65475 arabidopsis
1488	65.5	5.9	488	2	Q7UM74	Q7um74 rhodopirell
1489	65.5	5.9	492	2	Q8R3T2	Q8r3t2 mus musculu
1490	65.5	5.9	501	2	Q9AYA6	Q9aya6 oryza sativ
1491	65.5	5.9	506	1	SHS1_BOVIN	O46631 bos taurus
1492	65.5	5.9	507	2	Q8W4G6	Q8w4g6 arabidopsis
1493	65.5	5.9	508	2	O90423	O90423 pichinde ar
1494	65.5	5.9	508	2	Q9YTW9	Q9ytw9 pichinde ar
1495	65.5	5.9	508	2	Q9YTX1	Q9ytx1 pichinde ar
1496	65.5	5.9	509	2	Q766U5	Q766u5 avicennia m
1497	65.5	5.9	509	2	Q7YKM2	Q7ykm2 torenia vag
1498	65.5	5.9	513	2	Q8SM19	Q8sm19 tetranema m
1499	65.5	5.9	516	2	Q6CKH4	Q6ckh4 kluyveromyc
1500	65.5	5.9	521	2	Q98RM0	Q98rm0 guillardia

ALIGNMENTS

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RESULT 1
Q6UW07
ID   Q6UW07      PRELIMINARY;      PRT;   212 AA.
AC   Q6UW07;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   NX-17.
GN   ORFNames=UNQ678;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY359060; AAQ89419.1; -.
SQ   SEQUENCE   212 AA;  24024 MW;  C0AB61AB40BC3C15 CRC64;

  Query Match             100.0%;  Score 1102;  DB 2;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-93;
  Matches  212;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60

Qy         61 VPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLND 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLND 120

Qy        121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180

Qy        181 DAEDKCENMITIENGIPSDPLDMKGGILMMPS 212
              ||||||||||||||||||||||||||||||||
Db        181 DAEDKCENMITIENGIPSDPLDMKGGILMMPS 212


RESULT 2
Q9HBJ8
ID   Q9HBJ8      PRELIMINARY;      PRT;   222 AA.
AC   Q9HBJ8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
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```
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Collectrin (Transmembrane protein 27).
GN   Name=TMEM27;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21264468; PubMed=11278314; DOI=10.1074/jbc.M006723200;
RA   Zhang H., Wada J., Hida K., Tsuchiyama Y., Hiragushi K., Shikata K.,
RA   Wang H., Lin S., Kanwar Y.S., Makino H.;
RT   "Collectrin, a collecting duct-specific transmembrane glycoprotein, is
RT   a novel homolog of ACE2 and is developmentally regulated in embryonic
RT   kidneys.";
RL   J. Biol. Chem. 276:17132-17139(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow, Colon, and Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF229179; AAG09466.1; -.
DR   EMBL; BC014317; AAH14317.1; -.
DR   EMBL; BC015099; AAH15099.1; -.
DR   EMBL; BC050606; AAH50606.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
KW   Transmembrane.
SQ   SEQUENCE   222 AA;  25235 MW;  52C0ED522134ED05 CRC64;

  Query Match             97.4%;  Score 1073;  DB 2;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-90;
  Matches  206;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60

Qy         61 VPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLND 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 VPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLND 120

Qy        121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180

Qy        181 DAEDKCENMITIENGIPSDPLDMKGG 206
              ||||||||||||||||||||||||||
Db        181 DAEDKCENMITIENGIPSDPLDMKGG 206


RESULT 3
Q6AYY2
ID   Q6AYY2      PRELIMINARY;      PRT;   222 AA.
AC   Q6AYY2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Kidney-specific membrane protein.
GN   Name=Nx17;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Director MGC Project;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC078838; AAH78838.1; -.
SQ   SEQUENCE   222 AA;  25051 MW;  82716CBF4B6897D8 CRC64;

  Query Match             84.8%;  Score 935;  DB 2;  Length 222;
  Best Local Similarity   85.4%;  Pred. No. 6.1e-78;
  Matches  176;  Conservative   13;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
              ||| |||||| ||||||:| |||||||||||: ||||||| |||:|||||:|||||||||
Db          1 MLWALFFLVTTIHAELCRPDAENAFKVRLSIKAALGDKAYVWDTDEEYLFRAMVAFSMRK 60

Qy         61 VPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLND 120
              ||||| |||||||||||||||||||||| ||||||| |||||||||:||||:||||:|
Db         61 VPNREGTEISHVLLCNVTQRVSFWFVVTDPLKNHTLPAAEVQSAIRMNRNRINSAFFLDD 120

Qy        121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180
              |||||||||||||||||:|||:|||||||: ||||||:|||| ||||  | |  |:
Db        121 HTLEFLKIPSTLAPPMDPSVPVWIIVFGVIFCIVTVAIALLVLSGIRQRRRNKKGPPGVE 180

Qy        181 DAEDKCENMITIENGIPSDPLDMKGG 206
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                ||||||||:|||||||| ||||||||
Db        181 DAEDKCENIITIENGIPCDPLDMKGG 206


RESULT 4
Q9ESG4
ID   Q9ESG4      PRELIMINARY;      PRT;   222 AA.
AC   Q9ESG4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Collectrin (Transmembrane protein 27) (Mus musculus adult male kidney
DE   cDNA, RIKEN full-length enriched library, clone:0610008J07
DE   product:kidney-specific membrane protein, full insert sequence).
GN   Name=Tmem27; Synonyms=Nx17;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=99362608; PubMed=10432394;
RA   Zhang H., Wada J., Kanwar Y.S., Tsuchiyama Y., Hiragushi K., Hida K.,
RA   Shikata K., Makino H.;
RT   "Screening for genes up-regulated in 5/6 nephrectomized mouse
RT   kidney.";
RL   Kidney Int. 56:549-558(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ICR;
RX   MEDLINE=21264468; PubMed=11278314; DOI=10.1074/jbc.M006723200;
RA   Zhang H., Wada J., Hida K., Tsuchiyama Y., Hiragushi K., Shikata K.,
RA   Wang H., Lin S., Kanwar Y.S., Makino H.;
RT   "Collectrin, a collecting duct-specific transmembrane glycoprotein, is
RT   a novel homolog of ACE2 and is developmentally regulated in embryonic
RT   kidneys.";
RL   J. Biol. Chem. 276:17132-17139(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [9]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [10]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.;
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF178085; AAG09306.1; -.
DR   EMBL; BC049912; AAH49912.1; -.
DR   EMBL; AK002337; BAB22022.1; -.
DR   MGD; MGI:1926234; Tmem27.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
KW   Transmembrane.
SQ   SEQUENCE   222 AA;  25070 MW;  C07E732CE92935A9 CRC64;

  Query Match             84.2%;  Score 928;  DB 2;  Length 222;
  Best Local Similarity   84.5%;  Pred. No. 2.7e-77;
  Matches  174;  Conservative   15;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
              ||| |||||| |||||| | |||||||||||| ||||||| |||::||||:|||||||||
Db          1 MLWALFFLVTTIHAELCHPDAENAFKVRLSIRAALGDKAYVWDTDQEYLFRAMVAFSMRK 60

Qy         61 VPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLND 120
              ||||||||||||||||:|||||||||||||| |:|||| ||||||| |:||||:||||:|
```

```
Db         61 VPNREATEISHVLLCNITQRVSFWFVVTDPSNNYTLPAAEVQSAIRKNRNRINSAFFLDD 120

Qy        121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180
              ||||||||||||||:||||:|||:|||||||: ||||||:|||| |||| || |  |:
Db        121 HTLEFLKIPSTLAPPMEPSVPVWIIVFGVIFCIVTVAIALLVLSGIRQRRRNNKGPPGVE 180

Qy        181 DAEDKCENMITIENGIPSDPLDMKGG 206
              ||||||||:|||||||| ||||||||
Db        181 DAEDKCENIITIENGIPCDPLDMKGG 206


RESULT 5
Q9ESG3
ID   Q9ESG3      PRELIMINARY;      PRT;   222 AA.
AC   Q9ESG3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Collectrin.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=99362608; PubMed=10432394;
RA   Zhang H., Wada J., Kanwar Y.S., Tsuchiyama Y., Hiragushi K., Hida K.,
RA   Shikata K., Makino H.;
RT   "Screening for genes up-regulated in 5/6 nephrectomized mouse
RT   kidney.";
RL   Kidney Int. 56:549-558(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=21264468; PubMed=11278314; DOI=10.1074/jbc.M006723200;
RA   Zhang H., Wada J., Hida K., Tsuchiyama Y., Hiragushi K., Shikata K.,
RA   Wang H., Lin S., Kanwar Y.S., Makino H.;
RT   "Collectrin, a collecting duct-specific transmembrane glycoprotein, is
RT   a novel homolog of ACE2 and is developmentally regulated in embryonic
RT   kidneys.";
RL   J. Biol. Chem. 276:17132-17139(2001).
DR   EMBL; AF178086; AAG09307.1; -.
SQ   SEQUENCE   222 AA;  25226 MW;  7F4E166AE344F855 CRC64;

  Query Match             83.6%;  Score 921;  DB 2;  Length 222;
  Best Local Similarity   84.5%;  Pred. No. 1.2e-76;
  Matches  174;  Conservative   13;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
              ||| |||||| |||||||:| ||||||||||: ||||||| |||:|||||:|||||||||
Db          1 MLWALFFLVTTIHAELCRPDAENAFKVRLSIKAALGDKAYVWDTDEEYLFRAMVAFSMRK 60

Qy         61 VPNREATEISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLND 120
              ||||| |||||||||||||||||||||||| |||| ||||||||||||: |||:||||:|
Db         61 VPNREGTEISHVLLCNVTQRVSFWFVVTDPLKNHTFPAVEVQSAIRMNRKRINSAFFLDD 120

Qy        121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180
              ||||||||||||||||||||:|||:|||||||: ||||||:|||| ||||  | |  |:
Db        121 HTLEFLKIPSTLAPPMDPSVPVWIIVFGVIFCIVTVAIALLVLSGIRQRRRNKKGPPGVE 180

Qy        181 DAEDKCENMITIENGIPSDPLDMKGG 206
              ||||||||:|||||||| |||||| |
Db        181 DAEDKCENIITIENGIPCDPLDMKRG 206


RESULT 6
Q6PE94
ID   Q6PE94      PRELIMINARY;      PRT;   228 AA.
AC   Q6PE94;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC68634 protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Klein S., Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC058203; AAH58203.1; -.
SQ   SEQUENCE   228 AA;  25246 MW;  3A16B4B027E2E7E2 CRC64;

  Query Match             44.3%;  Score 488;  DB 2;  Length 228;
  Best Local Similarity   47.2%;  Pred. No. 9.4e-37;
  Matches   93;  Conservative   47;  Mismatches   55;  Indels    2;  Gaps    2;

Qy          1 MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK 60
              :|  |  | | :| :||:||:  | ||||:|: |||| || |:::|||||||::|| ||
Db          5 ILLFLLSLPTFVHGDLCEPGSRGALKVRLNIKAALGDNAYTWNSDEEYLFKAVMAFVMRS 64

Qy         61 VPNREATEISHVLLCNVTQRVSFWFVVTDPS-KNHTLPAVEVQSAIRMNKNRINNAFFLN 119
                 :  :||:::||| |:||||||||| || ::| :    |::|:|  :||||:|| ||
Db         65 YTKNDTFQISNIVLCNSTERVSFWFVVTSPSNESHPVSYSVVEAAVRNERNRINSAFLLN 124

Qy        120 DQTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNK-EPSE 178
              |:||||::|| ||||    |   |:|:|||:  :: |||| |::||: : |:: |    |
Db        125 DKTLEFVQIPPTLAPASQSSSSSWLIVFGVVVFVVSVAIAYLVVSGVIRHRKRLKSSEEE 184

Qy        179 VDDAEDKCENMITIENG 195
              ::| : :::  |:||
Db        185 SQNSEARMKSLDAIKNG 201


RESULT 7
Q6P0S0
ID   Q6P0S0      PRELIMINARY;      PRT;   235 AA.
AC   Q6P0S0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
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DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LOC402976 protein (Fragment).
GN   Name=LOC402976;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Strausberg R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC065470; AAH65470.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   235 AA;  26152 MW;  FB09C5A684D3BCC2 CRC64;

  Query Match             36.8%;  Score 405;  DB 2;  Length 235;
  Best Local Similarity   40.1%;  Pred. No. 4.3e-29;
  Matches   83;  Conservative   50;  Mismatches   70;  Indels    4;  Gaps    3;

Qy          2 LWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKV 61
              |  :  |   :  :||:  ::: ||||:|::||||: || |: :|::||:: :|::|||
Db         18 LLTIILLSPVVAQDLCKE-SKDGFKVRISLKTALGNDAYEWNESEKFLFRSTLAYAMRKK 76

Qy         62 PNREATEISHVLLCNVTQRVSFWFVVTDPS-KNHTLPAVEVQSAIRMNKNRINNAFFLND 120
                 :   | ::|:|| |:|||| |||| |:     :|  ||: |:| :|:|||||| |:|
Db         77 TGEDTYNIENILVCNDTKRVSFIFVVTLPADPTQLIPKEEVERAVRQSKHRINNAFLLSD 136

Qy        121 QTLEFLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVD 180
              ||||: :| ||| |:  : | |:|:|||:  |: | |  |::| : :|||   : :  |
Db        137 MTLEFVGVPPTLAVPIQYNTPPWLIVFGVVIGIVAVGIVALLMSTVSKRRRAKAKDAGFD 196

Qy        181 DAEDKCENMITIENGIPSDPLDMKGGI 207
                :|  :  |  |||     |: | |:
Db        197 --QDGDDEGIVKENGTALSGLNKKDGV 221


RESULT 8
Q9UFZ6
ID   Q9UFZ6      PRELIMINARY;      PRT;   804 AA.
AC   Q9UFZ6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein DKFZp434A014 (Fragment).
GN   Name=DKFZp434A014;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL110224; CAB53682.1; -.
DR   PIR; T14762; T14762.
DR   HSSP; Q10714; 1J37.
DR   MEROPS; M02.006; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   804 AA;  92340 MW;  91FF391074CB5DA9 CRC64;

  Query Match             34.1%;  Score 376;  DB 2;  Length 804;
  Best Local Similarity   47.9%;  Pred. No. 8.3e-26;
  Matches   79;  Conservative   32;  Mismatches   48;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::|||||||| |: || |||:: ||::||     || |:        |
Db        611 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 670

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |    :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        671 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTL 730

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPS 177
               ||  | | ||:|:|||:  :|:| | :|| :||  |::|||  |
Db        731 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARS 775


RESULT 9
Q9NRA7
ID   Q9NRA7      PRELIMINARY;      PRT;   805 AA.
AC   Q9NRA7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Angiotensin converting enzyme-like protein (Angiotensin I converting
DE   enzyme (Peptidyl-dipeptidase A) 2) (Angiotensin converting enzyme 2)
DE   (ACE-related carboxypeptidase ACE2).
GN   Name=ACE2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphoma;
RX   MEDLINE=20517872; PubMed=10924499; DOI=10.1074/jbc.M002615200;
RA   Tipnis S.R., Hooper N.M., Hyde R., Karran E., Christie G.,
RA   Turner A.J.;
RT   "A human homolog of angiotensin-converting enzyme. Cloning and
RT   functional expression as a captopril-insensitive carboxypeptidase.";
RL   J. Biol. Chem. 275:33238-33243(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
RA   Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
RA   Nickerson D.A.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
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RP   SEQUENCE FROM N.A.
RA   Douglas G.C., O'Bryan M.K., Hedger M.P., Yarski M.A., Smith A.I.,
RA   Lew R.A.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20429895; PubMed=10969042;
RA   Donoghue M., Hsieh F., Baronas E., Godbout K., Gosselin M.,
RA   Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,
RA   Breitbart R.E., Acton S.;
RT   "A novel angiotensin-converting enzyme-related carboxypeptidase (ACE2)
RT   converts angiotensin I to angiotensin 1-9.";
RL   Circ. Res. 87:E1-E9(2000).
DR   EMBL; AF241254; AAF78220.1; -.
DR   EMBL; AY217547; AAO25651.1; -.
DR   EMBL; AY623811; AAT45083.1; -.
DR   EMBL; AF291820; AAF99721.1; -.
DR   HSSP; Q10714; 1J37.
DR   MEROPS; M02.006; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR   GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   Carboxypeptidase.
SQ   SEQUENCE   805 AA;  92462 MW;  8EE6EB0A931550E8 CRC64;

  Query Match             34.1%;  Score 376;  DB 2;  Length 805;
  Best Local Similarity   47.9%;  Pred. No. 8.3e-26;
  Matches   79;  Conservative   32;  Mismatches   48;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::||||||| |: || |||:: ||::||    || |:        |
Db        612 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 671

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |   :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTL 731

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPS 177
                ||  | | ||:|:|||:  :|:| | :|| :||  |::|||  |
Db        732 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARS 776


RESULT 10
Q86WT0
ID   Q86WT0      PRELIMINARY;      PRT;   816 AA.
AC   Q86WT0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ACE2 protein (Fragment).
GN   Name=ACE2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC048094; AAH48094.1; -.
DR   PDB; 1R42; X-ray; A=-.
DR   PDB; 1R4L; X-ray; A=12-626.
DR   MEROPS; M02.006; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT   NON_TER       1      1
SQ   SEQUENCE   816 AA;  93516 MW;  EFBBD58B3DA2EDF3 CRC64;

  Query Match             34.1%;  Score 376;  DB 2;  Length 816;
  Best Local Similarity   47.9%;  Pred. No. 8.4e-26;
  Matches   79;  Conservative   32;  Mismatches   48;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::||||||| |: || |||:: ||::||    || |:        |
Db        623 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 682

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |   :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        683 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTL 742

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPS 177
                ||  | | ||:|:|||:  :|:| | :|| :||  |::|||  |
Db        743 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARS 787


RESULT 11
Q9BYF1
ID   Q9BYF1      PRELIMINARY;      PRT;   805 AA.
AC   Q9BYF1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ACE2.
GN   Name=ace2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suzuki Y., Watanabe M., Sugano S.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Komatsu T., Suzuki Y., Sugano S.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB046569; BAB40370.1; -.
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DR   HSSP; Q10714; 1J37.
DR   MEROPS; M02.006; -.
DR   Genew; HGNC:13557; ACE2.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004246; F:peptidyl-dipeptidase A activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   805 AA;  92490 MW;  D2AAB4C27088EB72 CRC64;

  Query Match             33.8%;  Score 373;  DB 2;  Length 805;
  Best Local Similarity   47.3%;  Pred. No. 1.6e-25;
  Matches   78;  Conservative   33;  Mismatches   48;  Indels    6;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
              | |: : |||:|:::||||:|| |: || |||:: ||::||    || |:         |
Db        612 PYADQSIKVRISLKSALGDRAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 671

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |   :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        672 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTL 731

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPS 177
               ||  | | ||:|:|||:  :|:| | :|| :||  |::|||  |
Db        732 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARS 776


RESULT 12
Q8R0I0
ID   Q8R0I0      PRELIMINARY;      PRT;   805 AA.
AC   Q8R0I0;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ace2 protein.
GN   Name=Ace2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026801; AAH26801.1; -.
DR   HSSP; Q10714; 1J37.
DR   MEROPS; M02.006; -.
DR   MGD; MGI:1917258; Ace2.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0004180; F:carboxypeptidase activity; TAS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ   SEQUENCE   805 AA;  92367 MW;  D8B883AAC966A8D9 CRC64;

  Query Match             32.8%;  Score 361;  DB 2;  Length 805;
  Best Local Similarity   40.9%;  Pred. No. 2e-24;
  Matches   81;  Conservative   35;  Mismatches   52;  Indels   30;  Gaps    5;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK---------VPNREATEI 69
              | |: : |||:|:::|||   || |  || :||:: ||::|||          ||  |
Db        612 PYADQSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMRKYFSIIKNQTVPFLE---- 667

Qy         70 SHVLLCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKI 128
                | : ::  ||||:| || |   :  :|  ||: ||||:: |||: | ||| :|||| |
Db        668 EDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFGLNDNSLEFLGI 727

Qy        129 PSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCEN 188
               ||  ||  | | ||:|||||:  :::| | :||::||  |::||:   |
Db        728 HPTLEPPYQPPVTIWLIIFGVVMALVVVGIIILIVTGIKGRKKKNETKRE---------- 777

Qy        189 MITIENGIPSDPLDMKGG 206
                ||  | | :|:  |
Db        778 ----EN--PYDSMDIGKG 789


RESULT 13
Q9D836
ID   Q9D836      PRELIMINARY;      PRT;   265 AA.
AC   Q9D836;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus adult male small intestine cDNA, RIKEN full-length
DE   enriched library, clone:2010305L05 product:ANIGOTENSIN-CONVERTING
DE   ENZYME-RELATED CARBOXYPEPTIDASE, full insert sequence.
DE   (Fragment).
GN   Name=Ace2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Small intestine;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Small intestine;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Small intestine;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
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RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Small intestine;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Small intestine;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Small intestine;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK008530; BAB25723.2; -.
DR   HSSP; Q10714; 1J37.
DR   MEROPS; M02.006; -.
DR   MGD; MGI:1917258; Ace2.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0004180; F:carboxypeptidase activity; TAS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   Pfam; PF01401; Peptidase_M2; 1.
KW   Carboxypeptidase.
FT   NON_TER       1      1
SQ   SEQUENCE   265 AA;  30078 MW;  2A02B2CE3817C76C CRC64;

  Query Match             32.4%;  Score 357;  DB 2;  Length 265;
  Best Local Similarity   44.1%;  Pred. No. 1.3e-24;
  Matches   75;  Conservative   33;  Mismatches   48;  Indels   14;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK---------VPNREATEI 69
              | |: : |||:|:::|||  || |  || :||:: ||::|||         ||  |
Db         72 PYADQSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMRKYFSIIKNQTVPFLE---- 127

Qy         70 SHVLLCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKI 128
                | : ::  ||||:| || |   :  :|  ||: |||||:: |||: | ||| :|||| |
Db        128 EDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFGLNDNSLEFLGI 187

Qy        129 PSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSE 178
              || ||  | | ||:|||||:  :::| | :||::||  |::||:   |
Db        188 HPTLEPPYQPPVTIWLIIFGVVMALVVVGIIILIVTGIKGRKKKNETKRE 237


RESULT 14
Q99N71
ID   Q99N71      PRELIMINARY;      PRT;   798 AA.
AC   Q99N71;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anigotensin-converting enzyme-related carboxypeptidase.
GN   Name=Ace2; Synonyms=ACE2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22375506; PubMed=12487024;
RA   Komatsu T., Suzuki Y., Imai J., Sugano S., Hida M., Tanigami A.,
RA   Muroi S., Yamada Y., Hanaoka K.;
RT   "Molecular cloning, mRNA expression, and chromosomal localization of
RT   mouse Angiotensin-converting Enzyme-Related Carboxypeptidase
RT   (mACE2).";
RL   DNA Seq. 13:217-220(2002).
DR   EMBL; AB053181; BAB40431.1; -.
DR   HSSP; Q10714; 1J37.
DR   MEROPS; M02.006; -.
DR   MGD; MGI:1917258; Ace2.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0004180; F:carboxypeptidase activity; TAS.
DR   InterPro; IPR001548; Peptidase_M2.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   InterPro; IPR001680; WD40.
DR   Pfam; PF01401; Peptidase_M2; 1.
DR   PRINTS; PR00791; PEPDIPTASEA.
DR   ProDom; PD004184; Peptidase_M2; 1.
DR   PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   Carboxypeptidase.
SQ   SEQUENCE   798 AA;  91943 MW;  403AEA29D55725A4 CRC64;

  Query Match             32.4%;  Score 357;  DB 2;  Length 798;
  Best Local Similarity   44.1%;  Pred. No. 4.6e-24;
  Matches   75;  Conservative   33;  Mismatches   48;  Indels   14;  Gaps    3;

Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRK---------VPNREATEI 69
              | |: : |||:|:::|||  || |  || :||:: ||::|||         ||  |
Db        612 PYADQSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMRKYFSIIKNQTVPFLE---- 667

Qy         70 SHVLLCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKI 128
                | : ::  ||||:| || |   :  :|  ||: |||||:: |||: | ||| :|||| |
Db        668 EDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFGLNDNSLEFLGI 727

Qy        129 PSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSE 178
              || ||  | | ||:|||||:  :::| | :||::||  |::||:   |
Db        728 HPTLEPPYQPPVTIWLIIFGVVMALVVVGIIILIVTGIKGRKKKNETKRE 777


RESULT 15
Q8IAQ8
ID   Q8IAQ8      PRELIMINARY;      PRT;  1053 AA.
AC   Q8IAQ8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vacuolar proton-translocating ATPase subunit A, putative.
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA   Quail M., Barrell B.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL844507; CAD51303.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
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DR   GO; GO:0015992; P:proton transport; IEA.
DR   InterPro; IPR002490; V_ATPase_sub116.
DR   Pfam; PF01496; V_ATPase_I; 1.
SQ   SEQUENCE   1053 AA;  122998 MW;  8B9F2559D3FC3F08 CRC64;

  Query Match             9.1%;  Score 100;  DB 2;  Length 1053;
  Best Local Similarity   21.3%;  Pred. No. 3;
  Matches   43;  Conservative   31;  Mismatches   72;  Indels   56;  Gaps    8;

Qy         22 ENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPNREATEISHVLLC------ 75
              |:| |    :|  : ||  |    |||    :         ||: :       | |
Db        330 EHAKKRLKELREIINDKEKALKAYEEYFINEIFVLINVVEPNKNSLIEEWKLFCKKERHI 389

Qy         76 ----------NVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAFFLNDQTL- 123
                       ::| |   |:   |  |  | |        |  : | : :|  |:|: |
Db        390 YNNLNYFEGSDITLRCDCWYSANDEEKIRHIL--------INKSSNDLVSALLLSDKILR 441

Qy        124 ------------EFLK----IPSTLAPP----MDPSVPIWI---IIFGVIF-------CI 153
                          || |    :  |   |    ::|::   |    :||:::       ||
Db        442 PNVSPPTYIKTNEFTKSYQSMVDTYGVPRYGEINPAISTIITFPFLFGIMYGDVGHGLCI 501

Qy        154 IIVAIALLILSGIWQRRRKNKE 175
              : |: |:|::   : :: | |
Db        502 FLFALFLIIMNNKVKNKKNNNE 523


Search completed: August 18, 2005, 17:37:39
Job time : 224 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2005, 17:28:18 ; Search time 16 Seconds
(without alignments)
1274.872 Million cell updates/sec

Title: US-09-997-641-387
Perfect score: 1102
Sequence: 1 MLWLLFFLVTAIHAELCQPG.....ENGIPSDPLDMKGGILMMPS 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	376	34.1	804	2	T14762	hypothetical prote
2	97.5	8.8	1086	2	T18523	integrin alpha cha
3	94	8.5	704	2	T29996	hypothetical prote
4	92.5	8.4	1153	2	T31080	nitric-oxide synth
5	89.5	8.1	244	2	E86471	unknown protein [i
6	89.5	8.1	793	2	D38992	cadherin 8 - human
7	89.5	8.1	1188	2	T13933	pol polyprotein -
8	89	8.1	1054	2	JC7294	alphaP integrin -
9	88	8.0	363	2	A37009	CD44 homolog membr
10	88	8.0	365	2	A34424	CD44 membrane glyc
11	86	7.8	362	2	A35616	T-cell surface gly
12	86	7.8	503	2	B38745	cell adhesion mole
13	85.5	7.8	667	2	T47482	receptor-like prot
14	84.5	7.7	468	2	E81924	probable two-compo
15	84.5	7.7	536	2	JG0022	flagellar basal-bo
16	84.5	7.7	1112	2	T28082	hypothetical prote
17	84	7.6	428	2	T48167	hypothetical prote
18	83.5	7.6	1337	1	I38670	protein-tyrosine-p
19	83	7.5	525	2	B83957	flagellar basal-bo
20	82.5	7.5	1044	2	S16516	integrin alpha-8 c
21	81.5	7.4	252	2	T05813	hypothetical prote
22	81.5	7.4	1048	2	A27421	integrin alpha-5 c
23	81	7.4	1041	2	T31437	integrin alpha cha
24	81	7.4	1135	2	I61186	alpha-7 integrin -
25	80.5	7.3	1034	2	A36108	integrin alpha-V c
26	80	7.3	234	1	QQBE43	membrane antigen g
27	80	7.3	489	2	AF2970	conserved hypothet
28	80	7.3	489	2	D98312	hypothetical prote
29	79.5	7.2	1044	2	T10050	integrin alpha-v c
30	79	7.2	437	2	S73284	hypothetical prote
31	79	7.2	2029	1	TDFFLK	protein-tyrosine-p
32	78.5	7.1	548	2	F71732	ABC transporter AT
33	78.5	7.1	836	2	T08424	tweety protein - f
34	78	7.1	343	2	A35639	G protein-coupled
35	78	7.1	377	2	AE0715	probable membrane
36	78	7.1	732	1	IJCHCB	B-cadherin precurs
37	78	7.1	1022	2	S49127	Na+/K+-exchanging
38	77.5	7.0	351	2	S45305	CD44 antigen precu
39	77.5	7.0	370	2	H64545	lipopolysaccharide
40	77.5	7.0	468	2	G81180	sensor histidine k
41	77.5	7.0	1499	2	I50212	protein-tyrosine-p
42	77	7.0	322	2	S75428	UDP-N-acetylglucos
43	77	7.0	366	2	A69063	O-antigen transpor
44	77	7.0	541	2	D97322	probable membrane-
45	77	7.0	1045	2	S60571	integrin alpha v c
46	76	6.9	180	2	A72758	hypothetical prote
47	76	6.9	306	2	D90519	hypothetical prote
48	76	6.9	369	2	H90587	hypothetical prote
49	76	6.9	542	2	T39474	amino acid permeas
50	76	6.9	614	2	B69332	conserved hypothet
51	76	6.9	771	2	T26176	hypothetical prote
52	76	6.9	1337	2	T38949	hypothetical prote
53	76	6.9	2251	2	T24490	hypothetical prote
54	76	6.9	2344	2	S64740	genome polyprotein
55	75.5	6.9	230	2	AF2237	hypothetical prote
56	75.5	6.9	255	1	S48146	mucin 1 precursor,
57	75.5	6.9	407	2	T08732	hypothetical prote
58	75.5	6.9	549	1	H65214	probable Na+/H+ ex
59	75.5	6.9	653	2	T25194	hypothetical prote
60	75.5	6.9	1344	1	A35175	mucin 1 precursor,
61	75	6.8	1007	2	PN0156	glutamate receptor
62	75	6.8	1008	2	S28858	glutamate receptor
63	74.5	6.8	549	2	C86100	hypothetical prote
64	74.5	6.8	549	2	G91259	hypothetical prote
65	74.5	6.8	631	2	I52257	episialin - mouse
66	74.5	6.8	664	2	T47481	receptor-like prot
67	74.5	6.8	2244	2	F90563	hypothetical prote
68	74	6.7	357	2	D45229	opsin, red-sensiti
69	74	6.7	589	2	F70033	glucan 1,4-alpha-m
70	73.5	6.7	321	2	AI1243	B. subtilis YqhQ p
71	73.5	6.7	465	2	S34929	probable membrane
72	73.5	6.7	488	2	T16402	hypothetical prote
73	73.5	6.7	599	2	T16774	hypothetical prote
74	73.5	6.7	624	2	D96494	protein F7F22.10 [
75	73.5	6.7	630	2	A39344	tumor-associated m
76	73.5	6.7	783	2	T30413	viral enhancing fa
77	73.5	6.7	796	2	I48277	cadherin-11 - mous
78	73.5	6.7	796	2	A53584	OB-cadherin precur
79	73.5	6.7	1166	2	H71609	hypothetical prote
80	73	6.6	304	2	AG3035	hypothetical prote
81	73	6.6	304	2	D98250	probable sugar ABC
82	73	6.6	315	2	T46993	hypothetical prote
83	73	6.6	381	2	S35940	class I histocompa
84	73	6.6	512	2	C64202	methionine-tRNA li
85	73	6.6	1181	2	A33998	integrin alpha-2 c
86	73	6.6	2344	2	S55399	genome polyprotein
87	72.5	6.6	231	2	T32953	hypothetical prote
88	72.5	6.6	299	2	I46690	CD80 precursor - r
89	72.5	6.6	682	2	T47473	receptor-like prot
90	72.5	6.6	2829	2	A42771	reticulocyte-bindi
91	72	6.5	283	1	FCMSG1	Fc gamma (IgG) rec
92	72	6.5	485	2	AG2531	hypothetical prote
93	72	6.5	543	2	T32109	hypothetical prote
94	72	6.5	1036	2	H64245	hypothetical prote
95	72	6.5	1106	2	S38783	integrin alpha cha
96	72	6.5	1447	2	T15200	hypothetical prote
97	72	6.5	5005	2	F82884	hypothetical prote
98	71.5	6.5	331	2	AC1256	E. coli LytB prote
99	71.5	6.5	453	2	C71518	probable permease
100	71.5	6.5	489	2	B53153	glucose transport
101	71.5	6.5	692	2	T05111	hypothetical prote
102	71.5	6.5	796	2	A38992	cadherin 11 precur

103	71.5	6.5	879	2	T02728	serine/threonine-s
104	71.5	6.5	936	2	B64567	cytochrome c bioge
105	71.5	6.5	1038	2	AG2187	hypothetical prote
106	71.5	6.5	1139	2	S28277	hypothetical prote
107	71	6.4	262	2	T27848	hypothetical prote
108	71	6.4	321	2	AE1606	B. subtilis YqhQ p
109	71	6.4	326	2	S54042	hypothetical prote
110	71	6.4	361	2	JH0417	cell adhesion mole
111	71	6.4	366	2	S53898	probable membrane
112	71	6.4	366	2	A53286	cell-surface glyco
113	71	6.4	395	2	I77371	CD44R5 - human
114	71	6.4	489	2	AI1276	multidrug-efflux t
115	71	6.4	489	2	AI1639	multidrug-efflux t
116	71	6.4	493	2	S13530	CD44E protein, epi
117	71	6.4	533	2	A72593	hypothetical prote
118	71	6.4	560	2	I38065	gene NMB protein -
119	71	6.4	627	2	H84693	probable protein k
120	71	6.4	685	2	T46843	H+/K+-exchanging A
121	71	6.4	685	2	G97351	K+-transporting AT
122	71	6.4	699	2	I37369	epican - human
123	71	6.4	742	2	A47195	lymphocyte homing
124	71	6.4	826	2	G97073	uncharacterized pr
125	71	6.4	1037	2	A60163	glycoprotein IIb -
126	71	6.4	1238	2	S68700	HPTP beta-like tyr
127	71	6.4	1262	1	B48758	protein-tyrosine-p
128	71	6.4	1496	1	A48758	protein-tyrosine-p
129	71	6.4	1501	2	I58148	protein-tyrosine-p
130	71	6.4	1863	2	S46217	protein-tyrosine-p
131	71	6.4	1907	2	S50893	protein-tyrosine-p
132	71	6.4	2344	1	RRWWRH	genome polyprotein
133	71	6.4	5138	2	B96695	hypothetical prote
134	70.5	6.4	129	2	I61187	alpha-7A integrin
135	70.5	6.4	516	2	T05940	cytochrome P450 83
136	70.5	6.4	584	2	T25059	hypothetical prote
137	70.5	6.4	900	2	T04839	protein kinase hom
138	70.5	6.4	1018	2	T19693	hypothetical prote
139	70.5	6.4	1027	1	PWCCNM	Na+/K+-exchanging
140	70.5	6.4	1139	2	T33275	hypothetical prote
141	70.5	6.4	1173	2	S48877	Ca2+-transporting
142	70.5	6.4	2672	2	A48126	translation activa
143	70	6.4	264	2	E72642	hypothetical prote
144	70	6.4	310	2	I64091	cell division prot
145	70	6.4	333	2	D88970	protein F15E11.11
146	70	6.4	362	2	A38545	hypothetical prote
147	70	6.4	402	2	A40678	T-cell adhesion re
148	70	6.4	489	1	RGBYP4	PET494 protein pre
149	70	6.4	544	2	H86828	fructuronate reduc
150	70	6.4	1039	2	A34269	integrin alpha-2b
151	70	6.4	1178	2	S44142	VLA-2 protein homo
152	70	6.4	1635	2	T32452	hypothetical prote
153	70	6.4	1636	2	S60403	probable membrane
154	70	6.4	1721	2	T21214	hypothetical prote
155	69.5	6.3	267	2	B84491	probable replicati
156	69.5	6.3	292	2	C95147	licB protein [impo
157	69.5	6.3	296	2	A98015	hypothetical prote
158	69.5	6.3	315	2	G98153	peptide ABC transp
159	69.5	6.3	315	2	AE3134	hypothetical prote
160	69.5	6.3	446	2	T45525	WSC4 homolog [impo
161	69.5	6.3	479	2	A98232	fructose-like PTS
162	69.5	6.3	481	2	H86078	PTS system, fructo
163	69.5	6.3	523	2	T05994	protein kinase hom
164	69.5	6.3	708	2	T43109	cytolysin B transp
165	69.5	6.3	900	2	T41607	probable vacuolar
166	69.5	6.3	900	2	T33482	hypothetical prote
167	69.5	6.3	1036	2	A42895	H+/K+-exchanging A
168	69.5	6.3	1072	2	T00041	BH-protocadherin P
169	69.5	6.3	1200	2	T00042	BH-protocadherin P
170	69	6.3	231	2	B83031	conserved hypothet
171	69	6.3	369	2	S33250	red visual pigment
172	69	6.3	401	2	H82175	multidrug resistan
173	69	6.3	616	1	VXZRNA	beta-1,2-glucan ex
174	69	6.3	728	2	A86453	CDS protein F9L11.
175	69	6.3	773	2	F90537	lipoprotein [impor
176	69	6.3	996	2	T18717	hypothetical prote
177	69	6.3	1017	2	A37227	Na+/K+-exchanging
178	69	6.3	1137	2	JC5950	integrin alpha-7 c
179	69	6.3	1408	2	T45039	hypothetical prote
180	68.5	6.2	141	2	T29781	hypothetical prote
181	68.5	6.2	275	2	T16312	hypothetical prote
182	68.5	6.2	330	2	S08500	QUTG protein - Eme
183	68.5	6.2	342	2	S33355	class I histocompa
184	68.5	6.2	348	2	D82252	RnfD-related prote
185	68.5	6.2	359	2	S20606	3-isopropylmalate
186	68.5	6.2	417	2	G64614	conserved hypothet
187	68.5	6.2	469	2	T34173	hypothetical prote
188	68.5	6.2	481	1	VGXPJV	surface glycoprote
189	68.5	6.2	485	2	S40843	phosphotransferase
190	68.5	6.2	511	2	AE2078	ferrichrome-iron r
191	68.5	6.2	564	2	E70394	ABC transporter (h
192	68.5	6.2	604	2	I36917	glycoprotein IIb -
193	68.5	6.2	796	2	I49556	cadherin-11 - mous
194	68.5	6.2	807	2	T24110	hypothetical prote
195	68.5	6.2	1025	2	S50293	probable membrane
196	68.5	6.2	1101	2	S51823	myosin heavy chain
197	68.5	6.2	1179	2	A53213	integrin alpha-E c
198	68.5	6.2	1192	2	A88925	protein F33E11.3 [
199	68	6.2	168	2	T31451	benzodiazepine rec
200	68	6.2	171	2	T41924	hypothetical prote
201	68	6.2	254	2	T18282	hypothetical prote
202	68	6.2	267	2	AI2794	conserved hypothet
203	68	6.2	297	2	E96002	probable sugar upt
204	68	6.2	310	2	H97573	hypothetical prote
205	68	6.2	318	2	H69959	hypothetical prote
206	68	6.2	342	2	AD3450	proline racemase (
207	68	6.2	362	2	A37783	iodopsin - chicken
208	68	6.2	399	2	AB0670	probable virulence
209	68	6.2	429	2	T29711	hypothetical prote
210	68	6.2	529	2	T22398	hypothetical prote
211	68	6.2	538	2	F90604	hypothetical prote
212	68	6.2	542	2	T19862	hypothetical prote
213	68	6.2	543	2	A28671	allantoate transpo
214	68	6.2	544	2	T32568	hypothetical prote
215	68	6.2	664	2	T10240	hypothetical prote
216	68	6.2	666	2	T10567	probable serine/th
217	68	6.2	691	2	D84889	probable receptor-
218	68	6.2	878	2	AH2075	ferrichrome-iron r
219	68	6.2	905	1	IJXLC1	N-cadherin 1 precu
220	68	6.2	905	2	S43064	cadherin - African
221	68	6.2	973	2	AH2762	ABC excinuclease s
222	68	6.2	982	2	G97543	excinuclease ABC c
223	68	6.2	1360	2	T31674	hypothetical prote
224	68	6.2	2321	2	S78549	notch3 protein - h
225	67.5	6.1	207	2	AC3381	hypothetical prote
226	67.5	6.1	270	1	S10532	interleukin-1 alph
227	67.5	6.1	278	2	A49266	fas ligand - rat
228	67.5	6.1	312	2	H71948	probable tetraacyl
229	67.5	6.1	330	2	C58931	NADH2 dehydrogenas
230	67.5	6.1	378	2	G70435	hypothetical prote
231	67.5	6.1	385	2	T24324	hypothetical prote
232	67.5	6.1	387	2	T15462	hypothetical prote
233	67.5	6.1	423	2	H75058	hypothetical prote
234	67.5	6.1	447	2	F82862	conjugal transfer
235	67.5	6.1	468	2	H75503	maltose ABC transp
236	67.5	6.1	489	2	C87480	conserved hypothet
237	67.5	6.1	497	2	A86146	hypothetical prote
238	67.5	6.1	589	2	F97735	hypothetical prote
239	67.5	6.1	608	2	H64473	hypothetical prote
240	67.5	6.1	612	2	B42755	E-selectin precurs
241	67.5	6.1	790	2	I51638	F-cadherin - Afric
242	67.5	6.1	1053	2	S44250	integrin alpha-5 c
243	67.5	6.1	1375	2	T13822	frazzled gene prot
244	67.5	6.1	1526	2	T13823	frazzled gene prot
245	67.5	6.1	1912	2	A56178	protein-tyrosine-p
246	67	6.1	220	1	RWHU28	T-cell surface gly
247	67	6.1	304	2	T22921	hypothetical prote
248	67	6.1	309	2	E71170	hypothetical prote

249	67	6.1	350	2	JN0621	G protein-coupled
250	67	6.1	364	1	OOHUR	opsin, red-sensiti
251	67	6.1	366	2	B96900	DNA polymerase III
252	67	6.1	413	1	IKEC5A	colicin V secretio
253	67	6.1	467	2	AB0279	probable virulence
254	67	6.1	477	2	E98024	hypothetical prote
255	67	6.1	479	2	C90128	hypothetical prote
256	67	6.1	506	2	H64618	sigma-54 interacti
257	67	6.1	614	2	T28930	hypothetical prote
258	67	6.1	650	2	B84526	hypothetical prote
259	67	6.1	705	2	T31261	hypothetical prote
260	67	6.1	717	2	T29816	hypothetical prote
261	67	6.1	748	2	A45243	envelope protein H
262	67	6.1	782	2	T43277	host cell factor 1
263	67	6.1	906	1	IJXLC2	N-cadherin 2 precu
264	67	6.1	956	2	JS0685	glutamate receptor
265	67	6.1	1023	1	S24650	Na+/K+-exchanging
266	67	6.1	1361	2	S50943	hypothetical prote
267	66.5	6.0	135	2	F83872	hypothetical prote
268	66.5	6.0	231	2	S06315	hypoxanthine phosp
269	66.5	6.0	364	2	I46604	MHC PD14 transplan
270	66.5	6.0	366	2	A60369	MHC class I histoc
271	66.5	6.0	366	2	I46603	MHC PD14a transpla
272	66.5	6.0	395	2	A48755	hyaluronan synthas
273	66.5	6.0	398	2	I49443	gene 2B4 protein -
274	66.5	6.0	419	2	A53100	hyaluronate syntha
275	66.5	6.0	425	2	T29617	hypothetical prote
276	66.5	6.0	482	2	E70450	UDP-MurNac-tripept
277	66.5	6.0	489	2	H91174	probable transport
278	66.5	6.0	489	2	H86020	probable transport
279	66.5	6.0	489	2	C65147	hypothetical 53.7
280	66.5	6.0	510	2	F84606	probable cytochrom
281	66.5	6.0	779	2	T31732	hypothetical prote
282	66.5	6.0	810	2	T33323	hypothetical prote
283	66.5	6.0	830	2	S25198	vacuolar membrane
284	66.5	6.0	1030	2	T18669	hypothetical prote
285	66.5	6.0	1081	2	T31329	receptor tyrosine
286	66.5	6.0	1136	2	T26953	hypothetical prote
287	66.5	6.0	1349	2	AI1476	cell surface prote
288	66.5	6.0	1371	2	T29019	hypothetical prote
289	66.5	6.0	1770	2	S56221	hypothetical prote
290	66	6.0	36	2	C45875	M1 class I histoco
291	66	6.0	179	2	E88028	protein F46F5.16 [
292	66	6.0	193	2	S73713	MG319 homolog H08_
293	66	6.0	226	2	T39298	hypothetical prote
294	66	6.0	250	2	I48850	TL antigen - mouse
295	66	6.0	252	2	G90513	hypothetical prote
296	66	6.0	260	2	T27266	hypothetical prote
297	66	6.0	267	2	B69461	hypothetical prote
298	66	6.0	284	2	E81421	probable periplasm
299	66	6.0	308	2	AI2601	conserved hypothet
300	66	6.0	311	2	T27203	hypothetical prote
301	66	6.0	328	2	A97384	hypothetical prote
302	66	6.0	357	2	A37440	red-sensitive visu
303	66	6.0	365	2	T22584	hypothetical prote
304	66	6.0	413	2	AD1068	probable sugar tra
305	66	6.0	477	2	E95158	hypothetical prote
306	66	6.0	480	2	T04849	protein kinase hom
307	66	6.0	503	1	QQXPGP	surface glycoprote
308	66	6.0	509	2	T06300	hypothetical prote
309	66	6.0	526	1	A32164	biliary glycoprote
310	66	6.0	539	2	D96562	unknown protein [i
311	66	6.0	545	2	T27614	hypothetical prote
312	66	6.0	572	2	T08509	trbL protein - Ent
313	66	6.0	623	2	D71435	hypothetical prote
314	66	6.0	631	2	JC6031	scaffoldin dockeri
315	66	6.0	654	2	E64245	periplasmic phosph
316	66	6.0	698	1	S31630	NAD+-protein ADP-r
317	66	6.0	705	2	T34531	hypothetical prote
318	66	6.0	710	2	T10654	hypothetical prote
319	66	6.0	735	2	T00850	probable receptor-
320	66	6.0	782	2	H90742	hypothetical prote
321	66	6.0	782	2	C85593	hypothetical prote
322	66	6.0	956	2	JH0826	glutamate ionotrop
323	66	6.0	1115	2	T09433	integrin alpha cha
324	66	6.0	1115	2	T09403	integrin alpha cha
325	66	6.0	1536	1	RGBYS3	regulatory protein
326	66	6.0	2089	2	C85426	ATM-like protein [
327	66	6.0	2160	2	T20241	hypothetical prote
328	66	6.0	3738	2	T05501	hypothetical prote
329	65.5	5.9	149	2	S73351	adhesin P1 homolog
330	65.5	5.9	215	2	A48463	Ras-like GTP-bindi
331	65.5	5.9	220	2	AH3231	conjugal transfer
332	65.5	5.9	231	2	JN0085	hypoxanthine phosp
333	65.5	5.9	271	2	H86166	protein F21B7.19 [
334	65.5	5.9	285	2	S36903	Fc gamma (IgG) rec
335	65.5	5.9	331	2	T21156	hypothetical prote
336	65.5	5.9	346	2	T24516	hypothetical prote
337	65.5	5.9	363	2	AE0516	3-isopropylmalate
338	65.5	5.9	413	2	T32831	hypothetical prote
339	65.5	5.9	417	2	JC4547	polysaccharide syn
340	65.5	5.9	435	2	T25350	hypothetical prote
341	65.5	5.9	450	2	T01711	probable serine/th
342	65.5	5.9	476	2	S64425	hypothetical prote
343	65.5	5.9	482	1	VGXPT7	surface glycoprote
344	65.5	5.9	485	2	T04840	hypothetical prote
345	65.5	5.9	521	2	A99100	phosphatidylinosit
346	65.5	5.9	543	2	B64232	transport system p
347	65.5	5.9	556	2	S51892	probable membrane
348	65.5	5.9	633	2	S62057	proline-rich prote
349	65.5	5.9	644	2	C81187	ABC transporter, A
350	65.5	5.9	644	2	C81916	probable ABC trans
351	65.5	5.9	709	2	S51793	dibasic processing
352	65.5	5.9	817	2	S53921	hypothetical prote
353	65.5	5.9	895	1	IJXLCP	EP-cadherin precur
354	65.5	5.9	906	1	VGBEC1	glycoprotein B pre
355	65.5	5.9	921	2	G71705	alkaline phosphata
356	65.5	5.9	936	2	H71862	probable cytochrom
357	65.5	5.9	1011	1	A45598	H+-exporting ATPas
358	65.5	5.9	1049	2	A27079	fibronectin recept
359	65.5	5.9	1056	2	T33167	hypothetical prote
360	65.5	5.9	1106	1	PFHUGB	platelet-derived g
361	65.5	5.9	1113	2	T26954	hypothetical prote
362	65.5	5.9	1348	2	AH1115	cell surface prote
363	65.5	5.9	1356	2	F84486	probable retroelem
364	65.5	5.9	1387	2	T16511	hypothetical prote
365	65.5	5.9	1738	2	C84507	hypothetical prote
366	65	5.9	108	2	B71074	hypothetical prote
367	65	5.9	199	2	A89774	superoxide dismuta
368	65	5.9	248	1	QQBE4L	probable glycoprot
369	65	5.9	249	2	S78186	H+-transporting tw
370	65	5.9	262	2	S56524	probable transcrip
371	65	5.9	295	2	A99489	arabinose ABC tran
372	65	5.9	330	2	A40071	Fc gamma (IgG) rec
373	65	5.9	330	2	I49660	Fc-gamma-1/gamma-2
374	65	5.9	357	2	T34012	hypothetical prote
375	65	5.9	445	2	H83272	sodium-translocati
376	65	5.9	467	2	T16319	hypothetical prote
377	65	5.9	478	2	T21144	hypothetical prote
378	65	5.9	482	2	C72254	glycerol kinase -
379	65	5.9	483	1	VGXPT5	surface glycoprote
380	65	5.9	483	1	VGXPTV	surface glycoprote
381	65	5.9	507	2	JC7883	cytochrome P450 4X
382	65	5.9	523	2	T49314	receptor lectin ki
383	65	5.9	611	2	T20501	hypothetical prote
384	65	5.9	630	1	BWBY	CBP2 protein - yea
385	65	5.9	637	2	JH0674	L-proline transpor
386	65	5.9	661	2	T39114	solute symporter f
387	65	5.9	673	2	S06048	poly(glycerol-phos
388	65	5.9	694	2	AI3022	potassium-transpor
389	65	5.9	718	2	A98262	H+/K+-exchanging A
390	65	5.9	737	2	T15615	hypothetical prote
391	65	5.9	745	2	T48366	anthranilate phosp
392	65	5.9	798	2	S01659	integrin beta-1 ch
393	65	5.9	799	1	IJMSFB	fibronectin recept
394	65	5.9	803	2	G96523	F11A17.8 [imported

395	65	5.9	855	2	S42621	protein-tyrosine k
396	65	5.9	1021	2	A28199	Na+/K+-exchanging
397	65	5.9	1023	2	A24414	Na+/K+-exchanging
398	65	5.9	1133	1	EGRT	epidermal growth f
399	65	5.9	1217	2	T22672	hypothetical prote
400	65	5.9	1365	2	T45031	hypothetical prote
401	65	5.9	1720	2	T07258	cell division prot
402	65	5.9	2809	2	T30213	G-cadherin - sea u
403	64.5	5.9	148	2	S40148	integrin alpha-7A
404	64.5	5.9	231	2	S06601	hypoxanthine phosp
405	64.5	5.9	232	2	H96698	hypothetical prote
406	64.5	5.9	240	2	H84497	probable replicati
407	64.5	5.9	270	2	I46620	interleukin-1 alph
408	64.5	5.9	314	1	B69954	penicillin toleran
409	64.5	5.9	344	2	I54445	MHC H2-Qa-Mb1 - mo
410	64.5	5.9	355	2	T14086	hypothetical prote
411	64.5	5.9	361	2	D53737	phosphate carrier
412	64.5	5.9	362	2	JH0290	class I histocompa
413	64.5	5.9	362	2	C53737	phosphate carrier
414	64.5	5.9	362	2	JQ2037	hypothetical 41K p
415	64.5	5.9	378	2	S00842	leukosialin precur
416	64.5	5.9	403	2	G83272	sodium-translocati
417	64.5	5.9	416	2	A82095	conserved hypothet
418	64.5	5.9	420	2	C64552	exonuclease VII, l
419	64.5	5.9	426	2	T45767	hypothetical prote
420	64.5	5.9	427	2	S44549	probable membrane
421	64.5	5.9	462	2	B57145	histidine kinase p
422	64.5	5.9	464	2	C30127	transmembrane carc
423	64.5	5.9	474	2	T01004	hypothetical prote
424	64.5	5.9	505	2	T28859	inward rectifier p
425	64.5	5.9	571	2	B89800	conserved hypothet
426	64.5	5.9	585	2	G86200	protein F12K11.15
427	64.5	5.9	662	2	S61193	probable membrane
428	64.5	5.9	700	2	T49445	adrenoleukodystrop
429	64.5	5.9	703	2	T24975	hypothetical prote
430	64.5	5.9	790	2	I50178	cadherin-6B - chic
431	64.5	5.9	826	2	C96694	hypothetical prote
432	64.5	5.9	859	1	VCLJST	env polyprotein pr
433	64.5	5.9	877	1	IJBOCN	N-cadherin precurs
434	64.5	5.9	906	1	IJHUCN	cadherin 2 precurs
435	64.5	5.9	906	1	IJMSCN	N-cadherin precurs
436	64.5	5.9	912	1	IJCHCN	N-cadherin precurs
437	64.5	5.9	913	1	IJCHCR	R-cadherin precurs
438	64.5	5.9	979	2	JH0589	glutamate receptor
439	64.5	5.9	979	2	JH0592	glutamate receptor
440	64.5	5.9	1036	2	T38734	hypothetical prote
441	64.5	5.9	1075	2	D70568	hypothetical prote
442	64.5	5.9	1338	2	T18287	protein-tyrosine k
443	64.5	5.9	1346	2	T17412	polyketide synthas
444	64	5.8	108	2	S40149	integrin alpha-7C
445	64	5.8	216	2	D70655	probable regulator
446	64	5.8	249	2	T16228	hypothetical prote
447	64	5.8	255	2	AD1159	flagellar biosynth
448	64	5.8	283	2	F88087	protein B0454.5 [i
449	64	5.8	285	2	H95943	probable sugar upt
450	64	5.8	288	2	B45897	MHC class I histoc
451	64	5.8	315	2	T37438	hemagglutinin - va
452	64	5.8	329	2	T23115	hypothetical prote
453	64	5.8	343	2	T03128	hypothetical prote
454	64	5.8	343	2	AI1143	hypothetical prote
455	64	5.8	372	2	S67770	probable membrane
456	64	5.8	380	2	S34964	rfc protein - Shig
457	64	5.8	389	2	S22839	translation activa
458	64	5.8	415	2	A35560	lysosomal membrane
459	64	5.8	421	2	D97078	MDR-type permease,
460	64	5.8	441	2	C86378	protein F21J9.6 [i
461	64	5.8	443	2	F85972	probable transport
462	64	5.8	443	2	G91127	probable transport
463	64	5.8	457	2	F83064	probable MFS trans
464	64	5.8	462	2	T04437	hypothetical prote
465	64	5.8	506	2	F71895	hypothetical prote
466	64	5.8	522	2	A31556	glucose transport
467	64	5.8	543	2	F84861	hypothetical prote
468	64	5.8	575	2	S46692	hypothetical prote
469	64	5.8	695	1	VHIWMV	nucleocapsid prote
470	64	5.8	716	2	T21516	hypothetical prote
471	64	5.8	754	2	A85043	probable LRR recep
472	64	5.8	769	2	F89870	serine proteinase
473	64	5.8	799	2	JC4126	integrin beta olig
474	64	5.8	819	2	A84504	Mutator-like trans
475	64	5.8	862	2	T05941	lipoxygenase (EC 1
476	64	5.8	865	2	C86639	preprotein translo
477	64	5.8	880	2	G90163	DNA-directed RNA p
478	64	5.8	1003	2	H82883	hypothetical prote
479	64	5.8	1013	1	S00801	Na+/K+-exchanging
480	64	5.8	1013	2	C24639	Na+/K+-exchanging
481	64	5.8	1020	2	A34474	Na+/K+-exchanging
482	64	5.8	1021	2	B24862	Na+/K+-exchanging
483	64	5.8	1022	1	S00503	Na+/K+-exchanging
484	64	5.8	1023	1	A24639	Na+/K+-exchanging
485	64	5.8	1070	2	E71401	probable selenium-
486	64	5.8	1168	2	T37496	probable pre-mRNA
487	64	5.8	1265	2	T21782	hypothetical prote
488	64	5.8	1398	2	T21884	hypothetical prote
489	64	5.8	1556	2	F96587	hypothetical prote
490	64	5.8	1898	2	S46216	leukocyte antigen-
491	64	5.8	2167	2	AF1489	cell wall-associat
492	64	5.8	2655	2	D96595	probable acetyl-Co
493	64	5.8	3890	2	C89921	hypothetical prote
494	63.5	5.8	117	2	G75135	hypothetical prote
495	63.5	5.8	192	2	A40606	superinfection exc
496	63.5	5.8	216	2	I76676	gene Ran protein -
497	63.5	5.8	244	2	AD1225	cobalamin biosynth
498	63.5	5.8	244	2	AF1578	cobalamin biosynth
499	63.5	5.8	244	2	G96507	hypothetical prote
500	63.5	5.8	247	2	S53863	H+-transporting tw
501	63.5	5.8	272	1	UHHU2	interleukin-2 rece
502	63.5	5.8	297	2	G87187	phosphoribosylamin
503	63.5	5.8	338	2	JC5435	aspartate-semialde
504	63.5	5.8	338	2	JC5436	aspartate-semialde
505	63.5	5.8	362	1	QQBED2	HHRF2 protein - hu
506	63.5	5.8	364	2	B85430	hypothetical prote
507	63.5	5.8	386	2	T39588	hypothetical prote
508	63.5	5.8	395	2	I52842	CD43 Lp-3 antigen
509	63.5	5.8	395	2	A43545	leukosialin CD43 p
510	63.5	5.8	423	2	A64486	dihydroorotase (EC
511	63.5	5.8	425	2	C65100	hypothetical 46.6
512	63.5	5.8	466	2	T32204	hypothetical prote
513	63.5	5.8	476	2	AF0191	probable sugar tra
514	63.5	5.8	492	1	C69762	di-tripeptide ABC
515	63.5	5.8	501	2	A86701	membrane-bound tra
516	63.5	5.8	508	2	A33378	fasciclin III prec
517	63.5	5.8	514	2	T29652	inward rectifier p
518	63.5	5.8	525	2	S49630	probable membrane
519	63.5	5.8	533	2	T46975	lysine-tRNA ligase
520	63.5	5.8	559	2	AF0891	probable exported
521	63.5	5.8	573	2	AB2401	hypothetical prote
522	63.5	5.8	605	2	G69060	threonine-tRNA lig
523	63.5	5.8	663	1	S30051	arachidonate 12-li
524	63.5	5.8	707	2	T30712	probable early tra
525	63.5	5.8	732	1	JU0132	acylaminoacyl-pept
526	63.5	5.8	820	2	A86510	leucyl tRNA synthe
527	63.5	5.8	820	2	C72113	leucine-tRNA ligas
528	63.5	5.8	830	2	T07824	1,4-alpha-glucan b
529	63.5	5.8	833	2	AB0448	probable insectici
530	63.5	5.8	863	2	C90482	ABC transporter, A
531	63.5	5.8	913	1	A47543	R-cadherin precurs
532	63.5	5.8	921	2	G02326	transcription fact
533	63.5	5.8	978	2	T16948	hypothetical prote
534	63.5	5.8	980	2	I57936	glutamate receptor
535	63.5	5.8	1051	2	A35761	cell surface glyco
536	63.5	5.8	1428	2	C85079	hypothetical prote
537	63.5	5.8	1628	2	T43682	nucleoporin - fiss
538	63.5	5.8	1691	1	D54689	protein-tyrosine-p
539	63.5	5.8	1894	2	C54689	protein-tyrosine-p
540	63.5	5.8	2403	2	T30875	PRP8 protein homol

541	63	5.7	98	2	T17086	NADH2 dehydrogenas
542	63	5.7	229	2	E95265	probable GntR-fami
543	63	5.7	253	2	T19129	hypothetical prote
544	63	5.7	289	2	C69346	hypothetical prote
545	63	5.7	299	2	G90386	conserved hypothet
546	63	5.7	310	2	G81381	probable integral
547	63	5.7	315	1	HNVZ4X	hemagglutinin prec
548	63	5.7	315	1	HNVZVT	hemagglutinin prec
549	63	5.7	330	2	A29915	teratocarcinoma gl
550	63	5.7	334	2	T11633	hypothetical prote
551	63	5.7	354	2	T09353	G protein-coupled
552	63	5.7	359	2	S24240	lymphocyte surface
553	63	5.7	361	2	T31815	hypothetical prote
554	63	5.7	362	2	A30901	lymphocyte adhesio
555	63	5.7	370	1	B35255	chloromuconate cyc
556	63	5.7	396	2	H69817	aminoacylase homol
557	63	5.7	411	2	A33664	96K lysosomal memb
558	63	5.7	452	2	D64961	membrane protein y
559	63	5.7	457	2	S13872	nicotinic acetylch
560	63	5.7	468	2	D84503	probable serine ca
561	63	5.7	497	2	G97738	histidine kinase s
562	63	5.7	498	2	AI0482	phosphate transpor
563	63	5.7	499	2	E91174	low-affinity phosp
564	63	5.7	499	2	E86020	low-affinity phosp
565	63	5.7	499	2	S47713	pitA protein - Esc
566	63	5.7	503	2	S54302	zinc transporter Z
567	63	5.7	553	2	B83714	iron (III) transpo
568	63	5.7	584	2	I50419	s-gicerin precurso
569	63	5.7	600	2	A47391	serum albumin prec
570	63	5.7	601	2	T47249	nuclear envelope p
571	63	5.7	610	2	T32327	hypothetical prote
572	63	5.7	663	2	T24881	hypothetical prote
573	63	5.7	673	2	F95079	conserved hypothet
574	63	5.7	673	2	A97947	conserved hypothet
575	63	5.7	694	2	JQ2383	glycoprotein H - h
576	63	5.7	698	1	S31714	NAD+-protein ADP-r
577	63	5.7	728	2	I65413	sodium-dependent n
578	63	5.7	730	2	I52632	sodium-dependent n
579	63	5.7	782	2	A64821	probable membrane
580	63	5.7	852	1	VCLJGG	env polyprotein pr
581	63	5.7	891	2	B82495	probable NADH dehy
582	63	5.7	996	2	JE0237	apolipoprotein E r
583	63	5.7	1010	2	B37227	Na+/K+-exchanging
584	63	5.7	1020	2	B24639	Na+/K+-exchanging
585	63	5.7	1021	1	PWSHNA	Na+/K+-exchanging
586	63	5.7	1021	1	S04630	Na+/K+-exchanging
587	63	5.7	1049	2	T42045	beta transducin-li
588	63	5.7	1226	2	T49915	pre-mRNA splicing
589	63	5.7	1379	1	S01254	hepatocyte growth
590	63	5.7	1394	2	A29637	position-specific
591	63	5.7	1642	2	T19130	hypothetical prote
592	63	5.7	2009	2	S49764	SEC7 protein - yea
593	62.5	5.7	169	2	S76351	hypothetical prote
594	62.5	5.7	171	2	F82340	thermoresistant gl
595	62.5	5.7	214	2	H86916	probable transcrip
596	62.5	5.7	216	2	S59942	GTP-binding protei
597	62.5	5.7	220	2	A84316	cobalamin biosynth
598	62.5	5.7	234	2	G64858	probable membrane
599	62.5	5.7	277	2	T23186	hypothetical prote
600	62.5	5.7	278	2	S46057	hypothetical prote
601	62.5	5.7	279	2	T09870	probable endo-xylo
602	62.5	5.7	295	2	AB3164	hypothetical prote
603	62.5	5.7	305	2	T27151	hypothetical prote
604	62.5	5.7	328	2	E86837	two-component syst
605	62.5	5.7	346	2	T11390	NADH2 dehydrogenas
606	62.5	5.7	351	2	AI2325	hypothetical prote
607	62.5	5.7	385	2	I46060	alpha-5 integrin s
608	62.5	5.7	386	1	JH0610	acid phosphatase (
609	62.5	5.7	398	2	T33513	hypothetical prote
610	62.5	5.7	418	2	S56369	hypothetical 44.8K
611	62.5	5.7	428	2	D86003	hypothetical prote
612	62.5	5.7	428	2	F91157	probable membrane
613	62.5	5.7	431	2	F90316	dsrP protein, prob
614	62.5	5.7	449	2	H88545	protein F59B2.13 [
615	62.5	5.7	451	2	T40736	probable pseudouri
616	62.5	5.7	474	2	T27006	hypothetical prote
617	62.5	5.7	475	2	T24850	hypothetical prote
618	62.5	5.7	480	2	T24422	amidophosphoribosy
619	62.5	5.7	493	1	ACRYB1	nicotinic acetylch
620	62.5	5.7	496	2	T52112	deoxyribodipyrimid
621	62.5	5.7	508	2	T41345	probable allantoat
622	62.5	5.7	519	2	S31133	hypothetical prote
623	62.5	5.7	531	2	T18931	hypothetical prote
624	62.5	5.7	588	2	B56636	retroid element PA
625	62.5	5.7	596	2	AC1318	two-component sens
626	62.5	5.7	635	2	S36718	phosphoprotein pho
627	62.5	5.7	645	2	E96631	probable receptor
628	62.5	5.7	669	2	D96006	probable cytochrom
629	62.5	5.7	672	2	A56765	sodium-glucose cot
630	62.5	5.7	695	2	G64327	H+-transporting tw
631	62.5	5.7	705	2	S70029	probable transmemb
632	62.5	5.7	721	2	JC7557	lipidosin - mouse
633	62.5	5.7	776	2	C96554	unknown protein [i
634	62.5	5.7	785	2	I50180	cadherin-7 - chick
635	62.5	5.7	789	2	I52701	K-cadherin - rat
636	62.5	5.7	790	2	I37016	cadherin-6 - human
637	62.5	5.7	802	2	B43735	bcsB protein - Ace
638	62.5	5.7	809	2	A57283	integrin beta chai
639	62.5	5.7	888	2	S23065	ufo protein - mous
640	62.5	5.7	894	1	A41527	protein-tyrosine k
641	62.5	5.7	907	1	VGBETE	glycoprotein B pre
642	62.5	5.7	1019	2	T13039	tyrosine kinase re
643	62.5	5.7	1095	2	G96746	hypothetical prote
644	62.5	5.7	1122	2	S64443	probable membrane
645	62.5	5.7	1213	2	T37959	hypothetical prote
646	62.5	5.7	1226	2	E84923	hypothetical prote
647	62.5	5.7	1333	2	A37488	Ras guanine nucleo
648	62.5	5.7	1391	2	T20642	hypothetical prote
649	62.5	5.7	1397	2	E87998	protein F09C3.1 [i
650	62.5	5.7	1592	2	S48933	probable transport
651	62.5	5.7	1896	2	T08851	Down syndrome cell
652	62.5	5.7	2229	2	T16199	hypothetical prote
653	62.5	5.7	2802	2	F97686	cyclic beta-(1-2)
654	62.5	5.7	2831	2	AI2911	beta (1->2) glucan
655	62	5.6	57	2	I47032	integrin alpha 5 -
656	62	5.6	100	2	H83987	hypothetical prote
657	62	5.6	144	2	S67078	probable membrane
658	62	5.6	255	2	AD1518	flagellar biosynth
659	62	5.6	263	2	T23347	hypothetical prote
660	62	5.6	269	2	F96506	hypothetical prote
661	62	5.6	277	2	B64548	conserved hypothet
662	62	5.6	289	2	S72554	melatonin receptor
663	62	5.6	290	2	S48301	geranylgeranyl tra
664	62	5.6	310	2	D71878	stress protein - H
665	62	5.6	311	2	E82468	hypothetical prote
666	62	5.6	312	2	AI0138	probable cation tr
667	62	5.6	318	2	H64687	magnesium and coba
668	62	5.6	318	2	F88102	protein W10G11.11
669	62	5.6	327	2	T10263	probable polygalac
670	62	5.6	353	2	A38421	opsin, green-sensi
671	62	5.6	368	2	B99563	hypothetical prote
672	62	5.6	375	2	T06096	hypothetical prote
673	62	5.6	376	2	F64208	oligopeptide trans
674	62	5.6	376	2	S48739	potassium channel
675	62	5.6	392	2	T29519	hypothetical prote
676	62	5.6	394	2	G85829	O antigen polymera
677	62	5.6	394	2	D90984	O antigen polymera
678	62	5.6	413	2	E96035	conserved hypothet
679	62	5.6	425	2	A64165	conserved hypothet
680	62	5.6	432	2	A43448	thrombin receptor
681	62	5.6	433	2	T17654	hypothetical prote
682	62	5.6	482	2	T27219	hypothetical prote
683	62	5.6	483	2	E64548	outer membrane pro
684	62	5.6	493	2	S68587	nicotinic acetylch
685	62	5.6	493	2	T24695	hypothetical prote
686	62	5.6	533	2	A71812	probable phosphate

687	62	5.6	560	2	S64091	probable membrane
688	62	5.6	592	2	B82498	sulfate permease f
689	62	5.6	613	2	JC7762	SOX-3 protein - gu
690	62	5.6	651	2	F90536	transport protein
691	62	5.6	656	2	A49579	amphotropic murine
692	62	5.6	660	2	S73673	hypothetical prote
693	62	5.6	662	2	G88451	protein K10D2.6 [i
694	62	5.6	669	2	T47484	receptor like prot
695	62	5.6	680	2	F95418	probable KdpB pota
696	62	5.6	732	1	MNXRW4	nonstructural prot
697	62	5.6	743	2	A97021	pyruvate-formate l
698	62	5.6	778	2	T05341	S-receptor kinase
699	62	5.6	790	2	G02678	cadherin-14 - huma
700	62	5.6	895	2	S20582	dystrophin-associa
701	62	5.6	916	2	T04752	aspartate kinase (
702	62	5.6	920	2	B84640	probable ligand-ga
703	62	5.6	932	2	T48489	receptor-like prot
704	62	5.6	938	2	B30111	alpha-adaptin C -
705	62	5.6	938	2	S11276	alpha-adaptin c -
706	62	5.6	1064	2	T01960	hypothetical prote
707	62	5.6	1073	2	B36429	integrin alpha-6 c
708	62	5.6	1169	2	H70178	exodeoxyribonuclea
709	62	5.6	1194	2	AE2041	two-component hybr
710	62	5.6	1236	1	A53970	1-phosphatidylinos
711	62	5.6	1247	2	T45743	hypothetical prote
712	62	5.6	1331	1	XORTDH	xanthine dehydroge
713	62	5.6	1656	2	S54520	probable membrane
714	62	5.6	1657	2	T19536	hypothetical prote
715	62	5.6	1692	2	G01449	probable mucin G2
716	62	5.6	2062	2	G96602	probable receptor
717	61.5	5.6	92	2	S03214	hypothetical prote
718	61.5	5.6	121	2	I46048	MHC class I antige
719	61.5	5.6	150	2	T33646	hypothetical prote
720	61.5	5.6	193	2	C91003	probable superinfe
721	61.5	5.6	204	2	H70008	hypothetical prote
722	61.5	5.6	212	1	VUQB3B	BabR protein 3 - B
723	61.5	5.6	216	1	TVHUC3	GTP-binding protei
724	61.5	5.6	216	2	S24031	GTP-binding protei
725	61.5	5.6	216	2	JC1455	GTP-binding protei
726	61.5	5.6	216	2	I57020	GTP-binding protei
727	61.5	5.6	225	2	T45889	hypothetical prote
728	61.5	5.6	284	2	A45840	MHC class I histoc
729	61.5	5.6	291	2	E82258	cell division prot
730	61.5	5.6	314	2	T15674	hypothetical prote
731	61.5	5.6	318	2	T11260	NADH2 dehydrogenas
732	61.5	5.6	326	2	T43219	serine/threonine-s
733	61.5	5.6	330	2	C95844	probable sugar ABC
734	61.5	5.6	334	2	E71103	probable aspartate
735	61.5	5.6	339	2	T29405	hypothetical prote
736	61.5	5.6	343	2	D89124	protein K07C11.2 [
737	61.5	5.6	345	2	S55377	urPAB protein prec
738	61.5	5.6	356	2	JH0289	class I histocompa
739	61.5	5.6	368	2	G86427	probable pectate l
740	61.5	5.6	393	2	G71173	hypothetical prote
741	61.5	5.6	394	2	C96500	hypothetical prote
742	61.5	5.6	399	2	AE0549	probable efflux pu
743	61.5	5.6	404	2	S34031	KTR3 protein - yea
744	61.5	5.6	413	2	T44804	type I site-specif
745	61.5	5.6	418	2	H86109	probable transport
746	61.5	5.6	418	2	B98269	probable transport
747	61.5	5.6	425	2	S33045	hypothetical prote
748	61.5	5.6	428	1	Q4ECAD	damX protein (aroB
749	61.5	5.6	457	2	S47938	amino-terminal ami
750	61.5	5.6	471	2	F72257	lipopolysaccharide
751	61.5	5.6	476	2	I80182	activin type I rec
752	61.5	5.6	487	2	I80183	activin type I rec
753	61.5	5.6	489	2	AD0988	probable PTR2 fami
754	61.5	5.6	502	2	B90103	T-complex protein
755	61.5	5.6	505	2	I53417	type I serine-thre
756	61.5	5.6	505	2	I38859	activin A receptor
757	61.5	5.6	511	2	B97783	aDP,ATP carrier pr
758	61.5	5.6	516	1	FWCNBB	beta-globulin B pr
759	61.5	5.6	528	2	T21834	hypothetical prote
760	61.5	5.6	531	2	A55788	glucuronosyltransf
761	61.5	5.6	544	2	AE1563	pyruvate dehydroge
762	61.5	5.6	568	2	E96648	hypothetical prote
763	61.5	5.6	578	2	H86365	T26J12.7 protein -
764	61.5	5.6	580	2	B84554	hypothetical prote
765	61.5	5.6	589	2	A71918	probable secretion
766	61.5	5.6	592	2	A96523	hypothetical prote
767	61.5	5.6	602	2	S60052	calcium-dependent
768	61.5	5.6	646	2	T28868	hypothetical prote
769	61.5	5.6	663	2	I52462	arachidonate 12-li
770	61.5	5.6	665	2	H87468	ubiquinol oxidase
771	61.5	5.6	675	2	D85065	receptor protein k
772	61.5	5.6	704	2	S25371	DBF4 protein - yea
773	61.5	5.6	715	2	G86634	hypothetical prote
774	61.5	5.6	740	2	F82614	conserved hypothet
775	61.5	5.6	783	2	I50116	N-cadherin precurs
776	61.5	5.6	825	1	A60386	interleukin-4 rece
777	61.5	5.6	826	2	G90283	hypothetical prote
778	61.5	5.6	846	2	T21700	hypothetical prote
779	61.5	5.6	865	2	T41909	hypothetical prote
780	61.5	5.6	936	2	S64384	probable membrane
781	61.5	5.6	968	2	T45746	hypothetical prote
782	61.5	5.6	1055	2	C82600	multidrug-efflux t
783	61.5	5.6	1379	2	S64603	YTA7 protein - yea
784	61.5	5.6	4969	2	A37113	ryanodine receptor
785	61	5.5	71	2	B83730	hypothetical prote
786	61	5.5	109	2	F82628	conserved hypothet
787	61	5.5	110	1	D38530	preprotein translo
788	61	5.5	110	2	AF0552	probable membrane
789	61	5.5	110	2	B90686	preprotein translo
790	61	5.5	110	2	F85536	preprotein translo
791	61	5.5	166	2	JC1348	hypothetical 18K p
792	61	5.5	207	2	T12097	GTP-binding protei
793	61	5.5	218	2	A43523	T-cell surface gly
794	61	5.5	230	2	F83697	ABC transporter (A
795	61	5.5	245	2	T18609	hypothetical prote
796	61	5.5	252	2	A69096	nitrogenase reduct
797	61	5.5	263	2	E72675	hypothetical prote
798	61	5.5	273	2	T37841	probable transloca
799	61	5.5	273	2	T31892	hypothetical prote
800	61	5.5	277	2	F71960	hypothetical prote
801	61	5.5	278	2	AB3413	signal peptidase I
802	61	5.5	288	2	G87319	hypothetical prote
803	61	5.5	290	2	T22161	hypothetical prote
804	61	5.5	299	2	T39602	conserved hypothet
805	61	5.5	300	2	AE2088	hypothetical prote
806	61	5.5	307	2	T39783	hypothetical prote
807	61	5.5	314	2	F83822	penicillin toleran
808	61	5.5	340	2	G64029	hypothetical prote
809	61	5.5	350	2	T25366	hypothetical prote
810	61	5.5	352	2	AF0692	probable membrane
811	61	5.5	355	2	H95320	NodI membrane tran
812	61	5.5	396	2	H84606	hypothetical prote
813	61	5.5	397	2	T08345	hypothetical prote
814	61	5.5	418	2	E91037	hypothetical prote
815	61	5.5	418	2	G85881	hypothetical prote
816	61	5.5	418	2	B65013	hypothetical prote
817	61	5.5	420	2	E72357	sugar ABC transpor
818	61	5.5	430	2	C72014	poly A polymerase
819	61	5.5	433	2	T31511	hypothetical prote
820	61	5.5	435	2	T19687	hypothetical prote
821	61	5.5	450	2	S35732	dnaA protein - Spi
822	61	5.5	461	2	S50864	avermectin-sensiti
823	61	5.5	461	2	S42084	basic protein - Cl
824	61	5.5	465	2	B55748	protein kinase (EC
825	61	5.5	482	2	G86227	hypothetical prote
826	61	5.5	499	2	A89015	protein B0213.10 [
827	61	5.5	501	2	A99319	transporter/facili
828	61	5.5	528	2	S57835	IgG-binding protei
829	61	5.5	531	2	S41986	26S proteasome reg
830	61	5.5	532	2	S27372	beta-fructofuranos
831	61	5.5	533	2	C64706	phosphate permease
832	61	5.5	536	2	H86192	hypothetical prote

833	61	5.5	574	2	S57072	hypothetical prote
834	61	5.5	579	1	WZBE34	gene 34 protein -
835	61	5.5	632	1	VGVNSY	surface glycoprote
836	61	5.5	681	2	T23811	hypothetical prote
837	61	5.5	689	2	F83843	hypothetical prote
838	61	5.5	712	2	D87418	proton pump, proba
839	61	5.5	721	2	S49789	hypothetical prote
840	61	5.5	749	2	T44796	DNA helicase pcrA
841	61	5.5	798	2	A28193	integrin beta-1 ch
842	61	5.5	798	2	B28193	integrin beta-1* c
843	61	5.5	822	2	S56801	hypothetical prote
844	61	5.5	834	2	JC7993	aryl hydrocarbon r
845	61	5.5	859	2	S24571	env protein - huma
846	61	5.5	895	2	A86410	protein F3M18.22 [
847	61	5.5	925	2	A55748	protein kinase (EC
848	61	5.5	976	2	A87576	peptidase, M16 fam
849	61	5.5	981	2	T18234	beta transducin ho
850	61	5.5	993	2	T25624	hypothetical prote
851	61	5.5	1006	2	AD2195	hypothetical prote
852	61	5.5	1012	2	T00958	hypothetical prote
853	61	5.5	1027	2	I38759	zinc finger/leucin
854	61	5.5	1146	2	S40311	integrin - fruit f
855	61	5.5	1273	1	TDRTLT	leukocyte common a
856	61	5.5	1472	2	S67195	probable membrane
857	61	5.5	1564	2	T27121	hypothetical prote
858	61	5.5	1729	2	S57596	ribosomal RNA proc
859	61	5.5	1858	2	T18273	1-phosphatidylinos
860	61	5.5	2051	2	T30938	receptor tyrosine
861	61	5.5	2102	2	T15626	hypothetical prote
862	61	5.5	2352	2	T43431	alpha-glucan synth
863	61	5.5	3944	2	T19997	hypothetical prote
864	60.5	5.5	87	2	E69071	hypothetical prote
865	60.5	5.5	87	2	G64328	hypothetical prote
866	60.5	5.5	152	2	S19388	probable membrane
867	60.5	5.5	172	2	S52801	hypothetical prote
868	60.5	5.5	179	2	H86211	protein F24B9.22 [
869	60.5	5.5	188	2	A34014	integrin alpha-3 c
870	60.5	5.5	196	2	AD2304	hypothetical prote
871	60.5	5.5	203	2	I49054	Ly-49G.2 antigen -
872	60.5	5.5	219	2	AB1115	hypothetical prote
873	60.5	5.5	222	2	A89776	capsular polysacch
874	60.5	5.5	259	2	G86962	probable membrane
875	60.5	5.5	259	2	A86822	hypothetical prote
876	60.5	5.5	267	2	I49053	Ly-49G.2 antigen -
877	60.5	5.5	280	2	I49052	Ly-49G.1 antigen -
878	60.5	5.5	305	2	C69609	cytochrome caa3 ox
879	60.5	5.5	323	2	F69454	signal-transducing
880	60.5	5.5	330	2	T29141	hypothetical prote
881	60.5	5.5	333	2	S78136	NADH2 dehydrogenas
882	60.5	5.5	334	2	T36052	probable cytochrom
883	60.5	5.5	340	2	A64902	peptide transport
884	60.5	5.5	343	2	H96703	probable RING zinc
885	60.5	5.5	347	2	E84898	hypothetical prote
886	60.5	5.5	356	2	G82938	hemin transport sy
887	60.5	5.5	357	2	S11133	class I histocompa
888	60.5	5.5	358	1	F64106	3-isopropylmalate
889	60.5	5.5	361	2	B27638	MHC class I histoc
890	60.5	5.5	365	2	I56053	class I histocompa
891	60.5	5.5	376	2	S57867	oncogene 1 - human
892	60.5	5.5	379	2	A82806	integral membrane
893	60.5	5.5	401	2	T14429	arginine decarboxy
894	60.5	5.5	403	2	A83344	hypothetical prote
895	60.5	5.5	407	2	S76637	hypothetical prote
896	60.5	5.5	413	2	AF0393	NADH2 dehydrogenas
897	60.5	5.5	418	2	E83686	hypothetical prote
898	60.5	5.5	420	2	E71955	exodeoxyribonuclea
899	60.5	5.5	429	2	T14524	S-locus-specific g
900	60.5	5.5	445	2	T23725	hypothetical prote
901	60.5	5.5	456	2	T24504	hypothetical prote
902	60.5	5.5	457	1	ACHUA1	nicotinic acetylch
903	60.5	5.5	463	2	AE1155	amino acid transpo
904	60.5	5.5	470	2	S39733	amino acid permeas
905	60.5	5.5	479	2	H97773	osmolarity sensor
906	60.5	5.5	497	2	T39680	probable allantoat
907	60.5	5.5	501	2	T36051	probable cytochrom
908	60.5	5.5	511	2	G64902	extreme acid resis
909	60.5	5.5	511	2	A90891	acid sensitivity p
910	60.5	5.5	511	2	H85726	acid sensitivity p
911	60.5	5.5	516	2	AB3088	MFS permease [prol
912	60.5	5.5	516	2	G98198	proline/betaine tr
913	60.5	5.5	529	2	S62468	probable membrane
914	60.5	5.5	537	2	T40507	probable vacuolar
915	60.5	5.5	543	2	A53790	cytochrome P450-EF
916	60.5	5.5	544	2	AF1206	pyruvate dehydroge
917	60.5	5.5	546	2	T24679	hypothetical prote
918	60.5	5.5	557	2	T22079	hypothetical prote
919	60.5	5.5	560	2	S27387	interferon alpha r
920	60.5	5.5	563	2	AD1019	probable sodium/hy
921	60.5	5.5	578	2	H82872	hypothetical prote
922	60.5	5.5	589	2	T38232	phenylalanine-tRNA
923	60.5	5.5	611	2	T28171	hypothetical prote
924	60.5	5.5	622	2	AG0952	membrane transport
925	60.5	5.5	622	2	T37257	hypothetical prote
926	60.5	5.5	636	2	JC5874	cellulase (EC 3.2.
927	60.5	5.5	637	2	T04552	hypothetical prote
928	60.5	5.5	662	2	D40228	neurexin II-beta p
929	60.5	5.5	694	2	H95012	hypothetical prote
930	60.5	5.5	702	2	C97884	hypothetical prote
931	60.5	5.5	722	2	F86233	hypothetical prote
932	60.5	5.5	737	2	T31349	hypothetical prote
933	60.5	5.5	751	2	C84367	DNA binding protei
934	60.5	5.5	767	2	B84594	probable LRR recep
935	60.5	5.5	786	2	S22155	oncogene 1 (tre-2
936	60.5	5.5	820	2	AE2130	ferrichrome-iron r
937	60.5	5.5	833	2	T24682	hypothetical prote
938	60.5	5.5	905	2	S56295	SAP155 protein - y
939	60.5	5.5	935	2	S66306	hypothetical prote
940	60.5	5.5	985	1	VCLJSP	env polyprotein -
941	60.5	5.5	1023	2	T31669	neural zinc finger
942	60.5	5.5	1051	2	A40021	integrin alpha-3 c
943	60.5	5.5	1069	2	T00043	BH-protocadherin-a
944	60.5	5.5	1170	2	I45914	integrin alpha 2 s
945	60.5	5.5	1259	2	G86119	hypothetical prote
946	60.5	5.5	1259	2	G91278	hypothetical prote
947	60.5	5.5	1715	2	C40228	neurexin II-alpha
948	60.5	5.5	2195	2	S61103	SEC16 protein - ye
949	60.5	5.5	2285	1	G02434	DNA-directed DNA p
950	60.5	5.5	2500	2	G88493	protein F57B9.2 [i
951	60.5	5.5	3649	1	S18268	delta-(L-alpha-ami
952	60	5.4	108	2	A86794	hypothetical prote
953	60	5.4	136	2	S04576	Ig heavy chain pre
954	60	5.4	195	2	C72252	conserved hypothet
955	60	5.4	234	2	S36116	proteasome endopep
956	60	5.4	237	2	C95199	nitroreductase fam
957	60	5.4	255	2	H81302	probable membrane
958	60	5.4	274	2	A47639	OX-2 membrane glyc
959	60	5.4	277	2	F83401	bacitracin resista
960	60	5.4	283	2	S27708	daunorubicin resis
961	60	5.4	285	2	D71105	hypothetical prote
962	60	5.4	286	2	F82881	hypothetical prote
963	60	5.4	288	2	T43353	nuclear receptor N
964	60	5.4	292	2	F69372	osmoprotection pro
965	60	5.4	297	2	T48855	probable heat shoc
966	60	5.4	302	2	H84731	hypothetical prote
967	60	5.4	305	2	C97762	ABC transporter pe
968	60	5.4	312	2	C64494	hypothetical prote
969	60	5.4	313	2	D70643	hypothetical prote
970	60	5.4	314	2	T21003	hypothetical prote
971	60	5.4	319	2	T33261	hypothetical prote
972	60	5.4	323	2	T27640	hypothetical prote
973	60	5.4	325	2	F86605	sulfite synthesis/
974	60	5.4	325	2	G72020	3'(2'),5'-bisphosp
975	60	5.4	329	2	T07401	peroxidase (EC 1.1
976	60	5.4	329	2	A40730	class I histocompa
977	60	5.4	331	2	C97493	malonyl-CoA-acyl c
978	60	5.4	331	2	AE2711	malonyl-CoA:acyl c

979	60	5.4	341	2	B75264	hypothetical prote
980	60	5.4	343	2	T01475	hypothetical prote
981	60	5.4	346	2	B86715	transcription regu
982	60	5.4	355	2	A64138	rfe protein - Haem
983	60	5.4	363	2	T28726	hypothetical prote
984	60	5.4	364	2	AG0581	probable aminotran
985	60	5.4	367	2	T22821	hypothetical prote
986	60	5.4	376	2	AF1943	multidrug-efflux t
987	60	5.4	397	2	D83311	conserved hypothet
988	60	5.4	406	2	T52647	hypothetical prote
989	60	5.4	412	2	T05703	calreticulin - bar
990	60	5.4	413	2	B83180	probable MFS trans
991	60	5.4	413	2	T34117	hypothetical prote
992	60	5.4	414	2	B81413	probable two-compo
993	60	5.4	415	2	T05705	calreticulin - bar
994	60	5.4	423	2	S39830	hypothetical prote
995	60	5.4	428	2	C96633	probable Serine/Th
996	60	5.4	443	2	T15704	hypothetical prote
997	60	5.4	452	2	T41108	transcription init
998	60	5.4	490	2	A64215	lysine-tRNA ligase
999	60	5.4	500	2	AE2032	glycerol kinase [i
1000	60	5.4	511	2	T27716	hypothetical prote
1001	60	5.4	512	2	E90442	hypothetical prote
1002	60	5.4	519	2	H96661	unknown protein, 5
1003	60	5.4	527	2	A53467	protein kinase SNF
1004	60	5.4	537	2	T33955	hypothetical prote
1005	60	5.4	540	2	G90068	choline transporte
1006	60	5.4	548	2	B90446	ABC transporter, p
1007	60	5.4	549	2	T16769	hypothetical prote
1008	60	5.4	582	2	A36190	penicillin-binding
1009	60	5.4	595	2	E69470	amino-acid ABC tra
1010	60	5.4	600	2	T24626	hypothetical prote
1011	60	5.4	628	2	AG1469	transporter homolo
1012	60	5.4	676	2	T24550	hypothetical prote
1013	60	5.4	687	2	S72932	hypothetical prote
1014	60	5.4	690	2	S75067	H+/K+-exchanging A
1015	60	5.4	690	2	A83441	potassium-transpor
1016	60	5.4	696	2	AB1566	hypothetical prote
1017	60	5.4	703	2	E69769	hypothetical prote
1018	60	5.4	709	2	A70624	H+/K+-exchanging A
1019	60	5.4	711	2	D83897	catalase katB [imp
1020	60	5.4	718	2	T05850	homeobox protein A
1021	60	5.4	756	2	AB1452	chitinase B homolo
1022	60	5.4	769	2	T22316	hypothetical prote
1023	60	5.4	773	2	I46059	beta-1 integrin su
1024	60	5.4	784	2	T45697	hypothetical prote
1025	60	5.4	792	2	T29187	hypothetical prote
1026	60	5.4	815	2	T15749	hypothetical prote
1027	60	5.4	819	2	T40527	hypothetical prote
1028	60	5.4	836	2	A90518	DNA polymerase III
1029	60	5.4	894	2	C86330	F6F9.22 protein -
1030	60	5.4	962	2	C43274	N-methyl D-asparta
1031	60	5.4	980	2	T49570	hypothetical prote
1032	60	5.4	995	2	T05842	hypothetical prote
1033	60	5.4	1013	2	C83771	hypothetical prote
1034	60	5.4	1072	2	T37742	serine threonine-p
1035	60	5.4	1091	2	A41543	integrin alpha-6 c
1036	60	5.4	1108	2	A48508	cyclic-nucleotide
1037	60	5.4	1136	2	A56559	enhancer-trap-locu
1038	60	5.4	1233	1	P3XRD3	major core protein
1039	60	5.4	1234	2	A34911	band 3-related pro
1040	60	5.4	1237	2	A31789	band 3-related pro
1041	60	5.4	1241	2	T37190	nephrin - human
1042	60	5.4	1250	1	B45219	N-methyl-D-asparta
1043	60	5.4	1253	2	T21065	hypothetical prote
1044	60	5.4	1254	2	T18425	hypothetical prote
1045	60	5.4	1290	2	A56493	leucocyte common a
1046	60	5.4	1338	2	T18416	hypothetical prote
1047	60	5.4	1358	1	XOCHDH	xanthine dehydroge
1048	60	5.4	1375	2	JT0345	dextransucrase (EC
1049	60	5.4	1465	2	S31262	TyB protein - yeas
1050	60	5.4	1492	2	T18560	DNA-directed DNA p
1051	60	5.4	1520	2	S46444	myosin MYA1, class
1052	60	5.4	1736	2	A29176	sex-limited protei
1053	60	5.4	1803	2	S56894	TyB protein - yeas
1054	60	5.4	2206	2	G71611	hypothetical prote
1055	60	5.4	2319	2	A47004	coagulation factor
1056	60	5.4	2523	2	T18477	hypothetical prote
1057	60	5.4	3011	1	S40770	genome polyprotein
1058	59.5	5.4	37	2	B45875	Tla class I histoc
1059	59.5	5.4	98	2	G81251	NADH2 dehydrogenas
1060	59.5	5.4	102	2	B34770	ORF2 protein - sai
1061	59.5	5.4	118	2	H90030	hypothetical prote
1062	59.5	5.4	141	2	B41543	integrin alpha-3A
1063	59.5	5.4	167	2	S14969	pathogenesis-relat
1064	59.5	5.4	179	2	T22143	hypothetical prote
1065	59.5	5.4	215	2	F96977	probable phosphata
1066	59.5	5.4	223	2	T19793	hypothetical prote
1067	59.5	5.4	231	2	A49265	flt3/flk-2 ligand
1068	59.5	5.4	235	2	I38440	flt3 ligand - huma
1069	59.5	5.4	236	2	AB3628	transcription regu
1070	59.5	5.4	237	2	C96737	unknown protein F3
1071	59.5	5.4	237	2	C81291	probable integral
1072	59.5	5.4	247	1	D24706	nodulation protein
1073	59.5	5.4	247	2	H95319	phosphoadenylyl-su
1074	59.5	5.4	267	2	I55686	LGL-1 - mouse
1075	59.5	5.4	280	2	I55577	Fc gamma (IgG) rec
1076	59.5	5.4	282	2	F90437	hypothetical prote
1077	59.5	5.4	302	2	F70220	conserved hypothet
1078	59.5	5.4	312	2	I78664	hypothetical 34.1K
1079	59.5	5.4	312	2	H91237	hypothetical prote
1080	59.5	5.4	312	2	D86085	hypothetical prote
1081	59.5	5.4	317	2	JL0118	Fc gamma (IgG) rec
1082	59.5	5.4	320	2	C88656	protein F56D6.5 [i
1083	59.5	5.4	323	2	B64504	methenyltetrahydro
1084	59.5	5.4	326	2	S59101	NADH2 dehydrogenas
1085	59.5	5.4	332	2	E86448	hypothetical prote
1086	59.5	5.4	344	2	S62765	NADH2 dehydrogenas
1087	59.5	5.4	345	1	QXMS2M	NADH2 dehydrogenas
1088	59.5	5.4	348	2	E64148	hypothetical prote
1089	59.5	5.4	359	1	HLHU12	MHC class I histoc
1090	59.5	5.4	360	2	T15639	hypothetical prote
1091	59.5	5.4	361	2	A75525	conserved hypothet
1092	59.5	5.4	382	1	F70116	hypothetical prote
1093	59.5	5.4	392	2	I54491	cell surface antig
1094	59.5	5.4	398	2	S07145	triacylglycerol li
1095	59.5	5.4	399	2	T27140	hypothetical prote
1096	59.5	5.4	408	2	C71520	hypothetical prote
1097	59.5	5.4	414	2	S48738	potassium channel
1098	59.5	5.4	415	2	T08191	translation elonga
1099	59.5	5.4	419	2	E83904	hypothetical prote
1100	59.5	5.4	424	2	H84134	multidrug resistan
1101	59.5	5.4	425	2	S52852	inward rectifier p
1102	59.5	5.4	427	2	D84540	hypothetical prote
1103	59.5	5.4	427	2	G02034	killer cell inhibi
1104	59.5	5.4	428	2	T03251	calnexin - maize (
1105	59.5	5.4	429	2	D82181	GGDEF family prote
1106	59.5	5.4	438	2	H91112	hypothetical prote
1107	59.5	5.4	438	2	H85957	partial probable t
1108	59.5	5.4	442	2	F87348	mannanase, probabl
1109	59.5	5.4	442	2	S49741	probable membrane
1110	59.5	5.4	456	2	S69677	hypothetical prote
1111	59.5	5.4	457	2	T21063	hypothetical prote
1112	59.5	5.4	463	2	AH1513	amino acid transpo
1113	59.5	5.4	478	2	T32476	probable protein-t
1114	59.5	5.4	484	2	S73490	glutamate-tRNA lig
1115	59.5	5.4	487	2	S65133	butyrophilin - mou
1116	59.5	5.4	501	2	B97790	aDP,ATP carrier pr
1117	59.5	5.4	502	2	I48241	ALK-1 - mouse
1118	59.5	5.4	502	2	JC4337	activin receptor l
1119	59.5	5.4	515	2	S20449	probable maturase,
1120	59.5	5.4	522	2	T28323	ORF MSV162 probabl
1121	59.5	5.4	564	2	S73615	threonine-tRNA lig
1122	59.5	5.4	564	2	AG2823	ABC transporter, m
1123	59.5	5.4	564	2	F97601	afub (AE006182) [i
1124	59.5	5.4	579	2	T15135	hypothetical prote

1125	59.5	5.4	580	2	B38418	jockey protein 1 -
1126	59.5	5.4	581	2	T06825	ketol-acid reducto
1127	59.5	5.4	591	1	S30145	ketol-acid reducto
1128	59.5	5.4	591	2	T45681	ketol-acid reducto
1129	59.5	5.4	606	2	T27072	hypothetical prote
1130	59.5	5.4	618	2	S06446	citrolysin-related
1131	59.5	5.4	621	1	D69295	endopeptidase La h
1132	59.5	5.4	638	2	T37309	flr-1 protein - Ca
1133	59.5	5.4	645	2	T28867	hypothetical prote
1134	59.5	5.4	652	2	I48083	amphotropic murine
1135	59.5	5.4	675	2	F84937	DNA ligase (NAD) (
1136	59.5	5.4	675	2	JC5898	beta-galactoside a
1137	59.5	5.4	687	2	T29220	hypothetical prote
1138	59.5	5.4	688	2	T33708	hypothetical prote
1139	59.5	5.4	730	2	T33041	hypothetical prote
1140	59.5	5.4	758	2	E81217	organic solvent to
1141	59.5	5.4	773	2	T46010	anthranilate phosp
1142	59.5	5.4	795	2	B97294	stage II sporulati
1143	59.5	5.4	802	2	B81794	probable solvent t
1144	59.5	5.4	823	2	A96501	hypothetical prote
1145	59.5	5.4	824	2	A86783	glycosyl transfera
1146	59.5	5.4	855	2	B75191	probable ATP-depen
1147	59.5	5.4	864	2	T05945	lipoxygenase (EC 1
1148	59.5	5.4	897	1	A39255	cytokine receptor
1149	59.5	5.4	942	2	S23251	protein-tyrosine k
1150	59.5	5.4	947	1	PXBY2P	H+-exporting ATPas
1151	59.5	5.4	974	2	T30204	pglZ protein - Str
1152	59.5	5.4	974	2	T35045	bacteriophage phiC
1153	59.5	5.4	998	2	T04214	hypothetical prote
1154	59.5	5.4	1000	2	F70368	cation efflux (Acr
1155	59.5	5.4	1038	2	T13177	sog protein - frui
1156	59.5	5.4	1053	2	I55534	VLA-3 alpha subuni
1157	59.5	5.4	1119	2	T18491	hypothetical prote
1158	59.5	5.4	1145	2	T13810	DNA-directed DNA p
1159	59.5	5.4	1187	1	A53661	protein-tyrosine-p
1160	59.5	5.4	1188	2	C71231	hypothetical prote
1161	59.5	5.4	1199	2	T23005	hypothetical prote
1162	59.5	5.4	1276	2	E96776	hypothetical prote
1163	59.5	5.4	1295	2	T21720	hypothetical prote
1164	59.5	5.4	1335	2	T18289	racGAP protein - s
1165	59.5	5.4	1467	2	PC1253	TyB protein - yeas
1166	59.5	5.4	1897	1	TDHULK	leukocyte antigen-
1167	59.5	5.4	2391	2	G89779	hypothetical prote
1168	59.5	5.4	2491	2	A57036	talin - slime mold
1169	59.5	5.4	2629	2	I46569	apolipoprotein B -
1170	59.5	5.4	4488	1	RRIHM2	genome polyprotein
1171	59.5	5.4	5147	1	IJFFTM	cadherin-related t
1172	59	5.4	118	2	F87479	conserved hypothet
1173	59	5.4	189	1	LPHUD	apolipoprotein D p
1174	59	5.4	202	2	T14970	phage lambda-relat
1175	59	5.4	219	2	T29732	hypothetical prote
1176	59	5.4	240	2	D64089	1-acylglycerol-3-p
1177	59	5.4	243	2	A89907	hypothetical prote
1178	59	5.4	247	2	E70137	cell division prot
1179	59	5.4	248	2	B45831	MHC class I histoc
1180	59	5.4	257	2	F86697	hypothetical prote
1181	59	5.4	260	2	B85181	FCA alpha and beta
1182	59	5.4	274	2	F96961	bacitracin resista
1183	59	5.4	285	2	T25971	hypothetical prote
1184	59	5.4	285	2	T24665	hypothetical prote
1185	59	5.4	289	2	B91042	N-acetylmuramoyl-l
1186	59	5.4	289	2	A36964	N-acetylmuramoyl-L
1187	59	5.4	289	2	E85886	N-acetylmuramoyl-l
1188	59	5.4	292	1	E64226	hypothetical prote
1189	59	5.4	308	2	CB1723	penicillin toleran
1190	59	5.4	313	2	T33849	hypothetical prote
1191	59	5.4	315	1	HNVZVV	hemagglutinin prec
1192	59	5.4	318	2	F72171	K9R protein - vari
1193	59	5.4	323	1	QQBED3	HHRF3 protein - hu
1194	59	5.4	323	2	JC2578	DNA repair protein
1195	59	5.4	325	2	T33549	hypothetical prote
1196	59	5.4	328	2	H87359	transcription regu
1197	59	5.4	329	2	T20094	hypothetical prote
1198	59	5.4	337	2	AD1414	cytochrome D ubiqu
1199	59	5.4	337	2	AC1790	cytochrome D ubiqu
1200	59	5.4	345	2	A97252	sporulation protei
1201	59	5.4	346	2	D97007	hypothetical prote
1202	59	5.4	348	2	T21627	hypothetical prote
1203	59	5.4	354	1	RGHUT2	GTP-binding regula
1204	59	5.4	358	2	F64136	rnfD protein homol
1205	59	5.4	366	2	A37374	Fc gamma (IgG) rec
1206	59	5.4	372	2	G96973	probable membrane
1207	59	5.4	372	2	AC3123	sugar acetylase [i
1208	59	5.4	372	2	D98164	hypothetical prote
1209	59	5.4	381	2	B71700	DNA polymerase III
1210	59	5.4	388	2	I69644	O-antigen polymera
1211	59	5.4	393	2	G71536	hypothetical prote
1212	59	5.4	396	2	A36339	FLO protein - gard
1213	59	5.4	403	2	T27948	hypothetical prote
1214	59	5.4	407	2	E88968	protein T27B7.4 [i
1215	59	5.4	418	2	A97220	probable membrane
1216	59	5.4	418	2	T52071	mRNA-binding prote
1217	59	5.4	431	2	B98162	hypothetical prote
1218	59	5.4	431	2	T16191	hypothetical prote
1219	59	5.4	445	2	D69939	conserved hypothet
1220	59	5.4	447	2	A47430	gastrin/cholecysto
1221	59	5.4	449	2	D86557	D-Ala/Gly permease
1222	59	5.4	449	2	A72067	d-ala/gly permease
1223	59	5.4	452	2	JC2459	gastrin/cholecysto
1224	59	5.4	453	2	T24127	probable chitinase
1225	59	5.4	455	2	E97081	amino acid permeas
1226	59	5.4	467	2	AG1059	probable membrane
1227	59	5.4	482	2	S63659	NADH2 dehydrogenas
1228	59	5.4	491	2	T22702	hypothetical prote
1229	59	5.4	497	2	C75618	hypothetical prote
1230	59	5.4	498	2	AG0988	probable low-affin
1231	59	5.4	501	2	T44298	sodium/proline sym
1232	59	5.4	509	2	A05183	hypothetical prote
1233	59	5.4	510	2	C85697	probable sporulati
1234	59	5.4	510	2	C90839	probable sporulati
1235	59	5.4	510	2	A64865	ycgB protein - Esc
1236	59	5.4	532	1	IFBY	beta-fructofuranos
1237	59	5.4	553	2	S64609	hypothetical prote
1238	59	5.4	563	2	S21043	cytochrome b6 homo
1239	59	5.4	571	2	T39378	probable FAD bindi
1240	59	5.4	576	2	A97239	MDR-type ABC trans
1241	59	5.4	595	2	AI0042	thiol,disulfide in
1242	59	5.4	613	2	T47483	receptor like prot
1243	59	5.4	623	2	T19876	hypothetical prote
1244	59	5.4	632	2	T45858	hypothetical prote
1245	59	5.4	664	2	C84747	probable protein k
1246	59	5.4	666	2	C90464	hypothetical prote
1247	59	5.4	670	2	T50312	hypothetical prote
1248	59	5.4	695	2	S44049	nucleocapsid prote
1249	59	5.4	782	2	S33945	late protein, 100K
1250	59	5.4	827	2	T39608	zinc finger transc
1251	59	5.4	833	2	S19087	gene Delta protein
1252	59	5.4	876	2	E89949	valine-tRNA ligase
1253	59	5.4	883	2	T18484	hypothetical prote
1254	59	5.4	968	2	T39908	probable coiled co
1255	59	5.4	1275	2	S65824	reverse transcript
1256	59	5.4	1323	2	S27224	N-methyl-D-asparta
1257	59	5.4	1323	2	I78557	N-methyl-D-asparta
1258	59	5.4	1352	2	G71051	probable ATP-depen
1259	59	5.4	1356	1	C45219	N-methyl-D-asparta
1260	59	5.4	1472	2	A84470	hypothetical prote
1261	59	5.4	1576	1	A23662	myosin I, high mol
1262	59	5.4	1658	2	D86890	DNA-directed DNA p
1263	59	5.4	1802	2	S52611	TyB protein - yeas
1264	59	5.4	2167	2	S19444	hypothetical prote
1265	59	5.4	4131	2	T21085	hypothetical prote
1266	59	5.4	4550	2	T18440	hypothetical prote
1267	58.5	5.3	162	2	T17051	NADH2 dehydrogenas
1268	58.5	5.3	162	2	T11802	NADH2 dehydrogenas
1269	58.5	5.3	176	2	AD0261	disulfide bond for
1270	58.5	5.3	176	2	G69163	hypothetical prote

1271	58.5	5.3	181	1	B44057	early E3 20.3K gly
1272	58.5	5.3	181	1	ERAD23	early E3 20.3K gly
1273	58.5	5.3	184	2	A36290	let-60 ras protein
1274	58.5	5.3	189	2	AF0372	glycine cleavage s
1275	58.5	5.3	203	2	AC1595	hypothetical prote
1276	58.5	5.3	237	2	AD1202	B. subtilis YvqF p
1277	58.5	5.3	249	2	AE0118	hypothetical prote
1278	58.5	5.3	250	2	H95161	conserved hypothet
1279	58.5	5.3	250	2	G98027	conserved hypothet
1280	58.5	5.3	252	2	AG1012	deoR family regula
1281	58.5	5.3	254	2	T28266	ORF MSV105 hypothe
1282	58.5	5.3	255	2	F84856	hypothetical prote
1283	58.5	5.3	260	2	S07169	cytochrome-c oxida
1284	58.5	5.3	264	2	S28969	N-carbamoylsarcosi
1285	58.5	5.3	266	2	G64022	hypothetical prote
1286	58.5	5.3	270	2	S09898	hypothetical prote
1287	58.5	5.3	273	2	C64589	hypothetical prote
1288	58.5	5.3	276	2	E97205	probable conserved
1289	58.5	5.3	290	2	S55116	hypothetical prote
1290	58.5	5.3	292	2	D71181	hypothetical prote
1291	58.5	5.3	296	2	D49539	xyloglucan endo-1,
1292	58.5	5.3	297	1	H64783	carbamate kinase (
1293	58.5	5.3	303	2	A40807	membrane glycoprot
1294	58.5	5.3	306	2	H87801	protein C10G11.3 [
1295	58.5	5.3	310	1	HNVZRA	hemagglutinin prec
1296	58.5	5.3	313	2	JQ1862	31R protein - vari
1297	58.5	5.3	313	2	H36854	hemagglutinin - va
1298	58.5	5.3	313	2	T28598	hypothetical prote
1299	58.5	5.3	316	2	S26715	hypothetical prote
1300	58.5	5.3	317	2	C83652	hypothetical prote
1301	58.5	5.3	327	2	S09566	replication initia
1302	58.5	5.3	330	2	F83955	flagellar motor sw
1303	58.5	5.3	334	2	A24455	repB protein - Bac
1304	58.5	5.3	335	2	AI3111	hypothetical prote
1305	58.5	5.3	335	2	D98175	hypothetical prote
1306	58.5	5.3	340	2	T28767	hypothetical prote
1307	58.5	5.3	343	2	AD1502	hypothetical prote
1308	58.5	5.3	344	1	RWRTC2	T-cell surface gly
1309	58.5	5.3	346	2	D85658	probable tellurium
1310	58.5	5.3	346	2	B99798	probable tellurium
1311	58.5	5.3	349	2	A53340	interferon regulat
1312	58.5	5.3	349	2	JC6311	interferon recepto
1313	58.5	5.3	352	2	H64919	probable membrane
1314	58.5	5.3	352	2	G85769	hypothetical prote
1315	58.5	5.3	352	2	C90921	hypothetical prote
1316	58.5	5.3	353	2	A87469	ubiquinol oxidase
1317	58.5	5.3	354	2	A83059	probable hemin deg
1318	58.5	5.3	356	2	S76018	hypothetical prote
1319	58.5	5.3	357	2	S11136	class I histocompa
1320	58.5	5.3	357	2	S11134	class I histocompa
1321	58.5	5.3	357	2	S11137	class I histocompa
1322	58.5	5.3	357	2	S11140	class I histocompa
1323	58.5	5.3	357	2	S11139	class I histocompa
1324	58.5	5.3	357	2	S11135	class I histocompa
1325	58.5	5.3	360	2	F90605	mannitol-1-phospha
1326	58.5	5.3	364	1	A64729	3-isopropylmalate
1327	58.5	5.3	364	2	I72217	class I histocompa
1328	58.5	5.3	365	2	I72218	class I histocompa
1329	58.5	5.3	372	2	G01425	nucleolar 75K auto
1330	58.5	5.3	373	2	JE0087	delta opioid recep
1331	58.5	5.3	377	2	H71081	hypothetical prote
1332	58.5	5.3	384	2	D97611	cell division prot
1333	58.5	5.3	384	2	AH2833	cell division prot
1334	58.5	5.3	384	2	AG0149	probable membrane
1335	58.5	5.3	393	2	E43674	US6 protein - huma
1336	58.5	5.3	393	2	B96780	hypothetical prote
1337	58.5	5.3	396	2	B91013	bicyclomycin resis
1338	58.5	5.3	396	2	D85857	bicyclomycin resis
1339	58.5	5.3	405	2	A96917	probable permease
1340	58.5	5.3	413	2	D95254	dltB protein [impo
1341	58.5	5.3	414	2	B98119	hypothetical prote
1342	58.5	5.3	423	2	I38979	inward rectifier p
1343	58.5	5.3	425	2	I48202	potassium channel-
1344	58.5	5.3	425	2	B64491	type I restriction
1345	58.5	5.3	430	2	S15147	hypothetical prote
1346	58.5	5.3	443	2	H98093	hemolysin [importe
1347	58.5	5.3	444	2	S41721	cell division cycl
1348	58.5	5.3	459	2	B70590	probable gorA prot
1349	58.5	5.3	467	2	T34617	NADH2 dehydrogenas
1350	58.5	5.3	479	2	C90457	cytochrome b558/56
1351	58.5	5.3	481	2	B70179	conserved hypothet
1352	58.5	5.3	490	2	A86265	Cytochrome P450 71
1353	58.5	5.3	492	2	S75049	hypothetical prote
1354	58.5	5.3	505	2	E87021	probable integral-
1355	58.5	5.3	519	2	F96517	hypothetical prote
1356	58.5	5.3	528	2	T31824	hypothetical prote
1357	58.5	5.3	538	2	T16034	hypothetical prote
1358	58.5	5.3	546	2	T06415	calnexin - soybean
1359	58.5	5.3	553	2	E91120	probable membrane
1360	58.5	5.3	553	2	E85965	probable membrane
1361	58.5	5.3	553	2	A65093	hypothetical prote
1362	58.5	5.3	555	2	T24671	hypothetical prote
1363	58.5	5.3	556	2	G90352	thermopsin precurs
1364	58.5	5.3	556	2	F82342	methyl-accepting c
1365	58.5	5.3	561	2	S63388	probable membrane
1366	58.5	5.3	570	2	AH1509	ABC transporter, A
1367	58.5	5.3	572	1	VGNZBA	cell fusion glycop
1368	58.5	5.3	574	1	VGNZBR	cell fusion glycop
1369	58.5	5.3	574	1	VGNZBS	cell fusion glycop
1370	58.5	5.3	574	2	JQ1583	cell fusion protei
1371	58.5	5.3	584	2	B86835	neopullulanase (EC
1372	58.5	5.3	586	2	JC6500	hnf-3/forkhead tra
1373	58.5	5.3	587	2	T46447	hypothetical prote
1374	58.5	5.3	588	2	B70618	probable PE protei
1375	58.5	5.3	607	2	H87286	ABC transporter, H
1376	58.5	5.3	611	2	T21747	hypothetical prote
1377	58.5	5.3	635	2	T22321	hypothetical prote
1378	58.5	5.3	661	2	D69907	hypothetical prote
1379	58.5	5.3	675	2	F85071	hypothetical prote
1380	58.5	5.3	711	1	ALBSXF	cyclomaltodextrin
1381	58.5	5.3	712	2	S23650	retrovirus-related
1382	58.5	5.3	729	2	T16522	hypothetical prote
1383	58.5	5.3	750	2	B90137	sulfate permease [
1384	58.5	5.3	769	2	T49911	anthranilate phosp
1385	58.5	5.3	770	2	T23999	hypothetical prote
1386	58.5	5.3	778	2	G71418	hypothetical prote
1387	58.5	5.3	783	2	S51968	probable membrane
1388	58.5	5.3	795	2	S26712	hypothetical prote
1389	58.5	5.3	807	2	S51460	hypothetical prote
1390	58.5	5.3	822	2	C97211	uncharacterized co
1391	58.5	5.3	848	2	G90128	elongation factor
1392	58.5	5.3	849	1	T09349	S-receptor kinase
1393	58.5	5.3	854	1	VCLJSI	env polyprotein pr
1394	58.5	5.3	874	1	QQBE15	BSLF1 protein - hu
1395	58.5	5.3	879	2	T19919	hypothetical prote
1396	58.5	5.3	896	2	AE1514	conserved membrane
1397	58.5	5.3	911	1	B3HU	band 3 anion trans
1398	58.5	5.3	918	1	PXBY1P	H+-exporting ATPas
1399	58.5	5.3	956	2	T23570	hypothetical prote
1400	58.5	5.3	964	2	E70826	probable membrane
1401	58.5	5.3	1030	2	T37868	probable helicase
1402	58.5	5.3	1131	2	F88570	protein K03H1.2 [i
1403	58.5	5.3	1144	2	T27408	hypothetical prote
1404	58.5	5.3	1147	2	S64930	serine/threonine-s
1405	58.5	5.3	1198	2	S51434	hypothetical prote
1406	58.5	5.3	1218	2	A88429	protein C28A5.2 [i
1407	58.5	5.3	1223	2	S43579	C28A5.1 protein (c
1408	58.5	5.3	1253	2	F86436	hypothetical prote
1409	58.5	5.3	1280	2	T29021	hypothetical prote
1410	58.5	5.3	1407	1	BWBYM1	TATA box-binding p
1411	58.5	5.3	1451	2	S41025	hypothetical prote
1412	58.5	5.3	1583	2	T00727	myosin heavy chain
1413	58.5	5.3	1717	2	T13961	DNA-directed RNA p
1414	58.5	5.3	1753	2	S30855	hypothetical prote
1415	58.5	5.3	2657	2	T18497	hypothetical prote
1416	58.5	5.3	4836	2	T14346	herc2 protein - mo

1417	58.5	5.3	4967	2	S72269	ryanodine receptor
1418	58.5	5.3	26926	1	I38344	titin, cardiac mus
1419	58	5.3	127	2	AG1425	hypothetical secre
1420	58	5.3	151	2	S48796	transforming prote
1421	58	5.3	153	2	A85848	hypothetical prote
1422	58	5.3	158	2	A27348	homeotic protein H
1423	58	5.3	171	2	C45665	adult-specific bru
1424	58	5.3	172	2	S52811	hypothetical prote
1425	58	5.3	172	2	A48775	major histocompati
1426	58	5.3	188	1	BVECTE	traE protein - Esc
1427	58	5.3	199	2	H75531	cytochrome c-type
1428	58	5.3	214	2	H96842	F23A5.34 [imported
1429	58	5.3	214	2	D96839	F23A5.5 [imported]
1430	58	5.3	218	2	AG3479	hypothetical prote
1431	58	5.3	218	2	T27678	hypothetical prote
1432	58	5.3	220	2	G90290	hypothetical prote
1433	58	5.3	232	2	AD0071	probable DedA-fami
1434	58	5.3	237	2	H83719	hypothetical prote
1435	58	5.3	239	2	A69124	hypothetical prote
1436	58	5.3	244	2	AH0363	probable membrane
1437	58	5.3	246	2	AD3574	brancheD-chain ami
1438	58	5.3	253	1	BVECCZ	probable sulfate t
1439	58	5.3	253	2	H85883	required for sulfa
1440	58	5.3	253	2	E91039	required for sulfa
1441	58	5.3	254	2	C81846	hypothetical prote
1442	58	5.3	260	1	A46517	CD27 antigen precu
1443	58	5.3	266	2	A86467	hypothetical prote
1444	58	5.3	269	2	F70377	shikimate 5-dehydr
1445	58	5.3	272	2	S59389	probable membrane
1446	58	5.3	275	2	C97028	probable metal-bin
1447	58	5.3	279	2	AH1540	transcription regu
1448	58	5.3	281	2	E72395	sugar ABC transpor
1449	58	5.3	286	2	G83211	conserved hypothet
1450	58	5.3	289	2	T28922	hypothetical prote
1451	58	5.3	289	2	AG0812	probable N-acetylm
1452	58	5.3	289	2	A53302	hemF 5'-region hyp
1453	58	5.3	290	4	S07060	opsin, red-sensiti
1454	58	5.3	296	2	T07367	thioredoxin-like p
1455	58	5.3	297	2	E83194	polyamine transpor
1456	58	5.3	299	1	A69962	phosphate butyrylt
1457	58	5.3	314	2	G69348	phosphate permease
1458	58	5.3	316	2	AI1935	hypothetical prote
1459	58	5.3	320	2	D64205	purine-nucleoside
1460	58	5.3	323	2	A82433	fructokinase VCA06
1461	58	5.3	332	2	AI2107	hypothetical prote
1462	58	5.3	336	2	S35934	matrix protein - m
1463	58	5.3	338	2	H84972	ornithine carbamoy
1464	58	5.3	342	1	HLHUC4	MHC class I histoc
1465	58	5.3	350	1	A37963	complement C5a ana
1466	58	5.3	355	2	I50091	visual pigment - M
1467	58	5.3	361	2	T30085	hypothetical prote
1468	58	5.3	364	1	OOHUG	opsin, green-sensi
1469	58	5.3	366	2	I37078	HLA-C alpha chain
1470	58	5.3	370	2	T44667	chloromuconate cyc
1471	58	5.3	370	2	JQ0176	chloromuconate cyc
1472	58	5.3	370	2	C90465	3-hydroxyacyl-CoA
1473	58	5.3	377	2	B97376	cytochrome ba(3) (
1474	58	5.3	385	2	H86627	hypothetical prote
1475	58	5.3	393	2	D97979	hypothetical prote
1476	58	5.3	394	2	H64448	polyferredoxin - M
1477	58	5.3	397	2	I48717	proteinase inhibit
1478	58	5.3	398	2	A99452	acyl-CoA dehydroge
1479	58	5.3	399	2	E86480	43.6K hypothetical
1480	58	5.3	409	2	G83871	multidrug-efflux t
1481	58	5.3	409	2	E97218	GGDEF domain conta
1482	58	5.3	409	2	T19688	hypothetical prote
1483	58	5.3	410	2	D91291	probable transport
1484	58	5.3	410	2	F86132	probable transport
1485	58	5.3	418	2	A97300	gamma-glutamyl pho
1486	58	5.3	419	2	S48077	K(ATP) channel - r
1487	58	5.3	430	2	D86611	poly A polymerase
1488	58	5.3	430	2	C81526	poly(A) polymerase
1489	58	5.3	439	2	C69392	hypothetical prote
1490	58	5.3	440	2	JL0144	interleukin-6 rece
1491	58	5.3	442	2	T04815	hypothetical prote
1492	58	5.3	447	2	T00425	photolyase/blue-li
1493	58	5.3	449	2	E87801	protein C10G11.6 [
1494	58	5.3	450	2	JQ1614	gastrin receptor -
1495	58	5.3	452	2	A46195	cholecystokinin B
1496	58	5.3	452	2	A85815	probable 2-compone
1497	58	5.3	452	2	B90967	probable 2-compone
1498	58	5.3	452	2	T00113	undecaprenyl-phosp
1499	58	5.3	452	2	C88969	protein F15E11.8 [
1500	58	5.3	453	2	S32817	gastrin receptor -

ALIGNMENTS

RESULT 1
T14762
hypothetical protein DKFZp434A014.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14762
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A;Reference number: Z18181
A;Accession: T14762
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-804 <WAM>
A;Cross-references: UNIPROT:Q9UFZ6; EMBL:AL110224
A;Experimental source: adult testis; clone DKFZp434A014
C;Genetics:
A;Note: DKFZp434A014.1

Query Match 34.1%; Score 376; DB 2; Length 804;
Best Local Similarity 47.9%; Pred. No. 1.8e-26;
Matches 79; Conservative 32; Mismatches 48; Indels 6; Gaps 3;

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Qy         19 PGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMR----KVPNREAT-EISHVL 73
                |: : |||:|:::||||||| |: || |||:: ||::||    || |:        |
Db        611 PYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVR 670

Qy         74 LCNVTQRVSFWFVVTDPSK-NHTLPAVEVQSAIRMNKNRINNAPFLNDQTLEFLKIPSTL 132
              : |:  |:|| | || |    :  :|  ||: ||||:::|||:|| ||| :|||| |  ||
Db        671 VANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTL 730

Qy        133 APPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPS 177
               ||  | | ||:|:|||:  :|:| | :|| :|  |::|||  |
Db        731 GPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARS 775
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RESULT 2
T18523
integrin alpha chain - Geodia cydonium
C;Species: Geodia cydonium
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18523
R;Pancer, Z.; Kruse, M.; Mueller, I.; Mueller, W.E.G.
Mol. Biol. Evol. 14, 391-398, 1997
A;Title: On the origin of adhesion receptors of metazoa: Cloning of the integrin alpha s
A;Reference number: Z18946; MUID:97254987; PMID:9100369
A;Accession: T18523
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1086 <PAN>
A;Cross-references: UNIPROT:O18428; EMBL:X97283; PIDN:CAA65943.1
C;Function:
A;Description: signal transduction
C;Superfamily: integrin alpha-4 chain

Query Match 8.8%; Score 97.5; DB 2; Length 1086;
Best Local Similarity 25.5%; Pred. No. 0.94;
Matches 36; Conservative 24; Mismatches 52; Indels 29; Gaps 6;

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Qy          63 NREATEISHVL----LCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFL 118
               ||   ||| |:    : :      |      ||       ||: :  :|::   :
Db         963 NRVQVEISAVIDERHIAGIDSYTFF------PSAQ-----VEMVGSDHINESNTKD---- 1007

Qy         119 NDQTLEFLKIPSTLAPPM-----DPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKN 173
               |: : ||  ||  |  |      | ||| ::|   :|  :|:: :  ::|      ||||
Db        1008 NNASAEFRSIPGELVVPSGSSGDDESVPWYVIAVPIIAAVILIIVVAVVLYFCGFFRRKN 1067

Qy         174 KEPSEVDDAEDKCENMITIEN 194
               |:     : ||:    :  ||
Db        1068 KQ-----EIEDQARENLAEEN 1083


RESULT 3
T29996
hypothetical protein C43H6.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29996
R;Le, T.T.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid C43H6.
A;Reference number: Z20717
A;Accession: T29996
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-704 <LET>
A;Cross-references: UNIPROT:Q18591; EMBL:U51999; PIDN:AAA96090.1; GSPDB:GN00028; CESP:C4
A;Experimental source: strain Bristol N2; clone C43H6
C;Genetics:
A;Gene: CESP:C43H6.9
A;Map position: X
A;Introns: 73/3; 143/3; 199/3; 349/2; 376/1; 422/2; 459/2; 523/1; 567/2; 635/2

  Query Match             8.5%;  Score 94;  DB 2;  Length 704;
  Best Local Similarity   25.6%;  Pred. No. 1.2;
  Matches   54;  Conservative   36;  Mismatches   69;  Indels   52;  Gaps   13;

Qy          38 KAYAWD-------TNE-EYLFKAMVAFSMRKVPNR------------EATEISHVLL--C 75
               |   ||        ||   |: :: :  :|    :|            :|||| :  |  |
Db         477 KLAVWDYPVSDKFTNMWRYMQESKLPVNMDTAVDRVLNSVDGFAFIGDATEIKYAALTNC 536

Qy          76 NVTQRVSFWFVVTDPSKNHTLP-AVEVQSAIRMNKNRINNA--FFLNDQTLEFLK----- 127
               |: |       | |: |:    | |: |||   : |::|::|    ||:: || ||
Db         537 NLQQ------VGTEFSRK---PYAIAVQSG-HILKDKISSAILMLLNERRLETLKEKWWT 586

Qy         128 -IPSTLAPP--MDPSVPIWIIIFGVIFCIIIVAIALLILS-----GIWQRRRKNKEPSEV 179
                |: :: |   | |  | |  | :| :|:  ||| |::       ::|: :      |
Db         587 DNPNKVSCPDSSDESDGISIQNIGGVFIVILAGIALSIVTLAFEYYYYKRKARKAAEKEQ 646

Qy         180 DDAEDKCENMITIE----NGIPSDPLDMKGG 206
               :: | |    :       ||:  |   :  |
Db         647 EELEMKQSQQVVPNGFHTNGVKQDAPKLTNG 677


RESULT 4
T31080
nitric-oxide synthase (EC 1.14.13.39) - great pond snail
C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31080
R;Korneev, S.A.; Piper, M.R.; Picot, J.; Phillips, R.; Korneeva, E.I.; O'Shea, M.
J. Neurobiol. 35, 65-76, 1998
A;Title: Molecular characterization of NOS in a mollusc: expression in a giant modulator
A;Reference number: Z20970; MUID:98211896; PMID:9552167
A;Accession: T31080
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1153 <KOR>
A;Cross-references: UNIPROT:O61309; EMBL:AF012531; NID:g3158018; PID:g3158019; PIDN:AAC1
C;Genetics:
A;Gene: NOS
C;Function:
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH t
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reducta
C;Keywords: FAD; flavoprotein; FMN; heme; iron; metalloprotein; NADP; oxidoreductase; pho
F;82/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             8.4%;  Score 92.5;  DB 2;  Length 1153;
  Best Local Similarity   21.1%;  Pred. No. 2.9;
  Matches   64;  Conservative   28;  Mismatches   76;  Indels  135;  Gaps   13;

Qy          21 AENAFKVRLSIRTALGDKAYAWDTNEEYLFKA-MVAFSMRKVPNRE---ATEI------- 69
               | ||      :: | ||    :  |   :  | :|     | |: :    |||
Db         689 AHNA----TDLKYAPGDHVAIFPANSPEIVDAILVRLDTSKGPSPDQVVKTEISTQLGTN 744

Qy          70 ----SHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRI-----NNAFF--- 117
                   ||: :|      ||   || |      |  :  |::  |:|:::     |:  :
Db         745 DTWRSHLPICTSRTAFSFLLDVTTPPSQEILQVLATQASSDMDKHKLEQLASNSEAYEKW 804

Qy         118 ---LNDQTLEF------LKIPSTL---------------------------------- 132
                  |:   ||       |||| :|
Db         805 RLDLSPNILEILDEFPSLKIPPSLLLTQLPLLQPRYYSISSSQQKNPNEVHATIAVVRFK 864

Qy         133 --------------------------------AP----PMDPSVPIWIIIFGVIFCIIIV 156
                                               ||    | |||:|| :|  |
Db         865 TQDGDGPVHEGVCSSWLNRSPIGTVVPCFLRSAPHFHLPEDPSLPIIMIGPG-------- 916

Qy         157 AIALLILSGI------WQRRRKNKEPSEVDDAEDKCEN-MITIENGIPSDPLDMKGGILM 209
                   |||       ||:|      |:::    ||| |:: |  |||    |
Db         917 -------SGIAPFRSFWQQRL-----GEIENTMPSCENTMLSCETTIPSCENSMPSCENT 964

Qy         210 MPS 212
               |||
Db         965 MPS 967


RESULT 5
E86471
unknown protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86471
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86471
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-244 <STO>
A;Cross-references: UNIPROT:Q9C6E1; GB:AE005172; NID:g11386315; PIDN:AAG35106.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: Arabidopsis thaliana hypothetical protein F7M19.50

  Query Match             8.1%;  Score 89.5;  DB 2;  Length 244;
  Best Local Similarity   24.7%;  Pred. No. 0.9;
  Matches   39;  Conservative   30;  Mismatches   52;  Indels   37;  Gaps    9;

Qy           3 WLLFFLVTAIHAELCQPGAENAFKVRL--------SIRTALGDK--AYAWDTNEEYLFKA 52
               | :  :|  |: ::   |   |||::||          |   :| :  |: :|  :|  :|
Db          17 WTICVMVLRIYKKILNP---NAFELRLVLADEWGTQIEATIGPRFSAFYFDRIKENQWKT 73

Qy          53 MVAFSMRKVPNREATE----------ISHVLLCNVTQR--------VSFWFVVTDPSKNH 94
               :  | :|  || || :          : | :: : | |          | ::| |   |
Db          74 ITTFLVR--PNCEAIKTTPHQFRILFMDHTIVTSSTPRETGLLNKFTPFDYIVDDVVGND 131
```

```
Qy          95 TLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPSTL 132
               ||  |:|  |: :|   : |    |:  :   |:| |:
Db         132 TL--VDVIGAL-VNVGIMTNT-ASNENDMAGFKLPFTI 165
```

RESULT 6
D38992
cadherin 8 - human
C;Species: Homo sapiens (man)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
C;Accession: D38992
R;Suzuki, S.; Sano, K.; Tanihara, H.
Cell Regul. 2, 261-270, 1991
A;Title: Diversity of the cadherin family: evidence for eight new cadherins in nervous t
A;Reference number: S24305; MUID:91283540; PMID:2059658
A;Accession: D38992
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-793 <SUZ>
A;Cross-references: GB:L34060; NID:g506411; PIDN:AAA35628.1; PID:g506412
C;Genetics:
A;Gene: GDB:CDH8
A;Cross-references: GDB:5822911
C;Superfamily: cadherin; cadherin repeat homology
C;Keywords: calcium binding; cell adhesion; duplication
F;163-269/Domain: cadherin repeat homology <CDH>

 Query Match 8.1%; Score 89.5; DB 2; Length 793;
 Best Local Similarity 20.6%; Pred. No. 3.6;
 Matches 50; Conservative 35; Mismatches 93; Indels 65; Gaps 10;

```
Qy          13 HAELCQPGAENAFKVRLSIRTALGDKAYAWDT---------NEEYLFKAMVAFSMRKVPN 63
               | :| :    ||   :::: | |  :   |          |   : :  ||  :  | |
Db         425 HTDLERQFNINADDGKITLATPLDRELSVWHNITIIATEIRNHSQISRVPVAIKVLDV-N 483

Qy          64 REATEIS---HVLLC------NVTQRVSFWFVVTDPSKNH-----TLPAVEVQSAIRMNK 109
                 | | :      ||       | | ||      ||   |      || :       : |
Db         484 DNAPEFASEYEAFLCENGKPGQVIQTVSA-MDKDDPKNGHYFLYSLLPEMVNNPNFTIKK 542

Qy         110 NRINNAFFL------NDQTLEFLKIPSTLA----PPMDPSVPIWIIIFG---------- 148
               |  |:   |      | | |   :|  ::    ||:  :  : | : |
Db         543 NEDNSLSILAKHNGFNRQKQEVYLLPIIISDSGNPPLSSTSTLTIRVCGCSNDGVVQSCN 602

Qy         149 -----------------VIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCENMIT 191
                              :: |||:: : :::   :  || :  ||  : | ||  ||:|
Db         603 VEAYVLPIGLSMGALIAILACIILLLVIVVLF--VTLRRHQKNEPLIIKDDEDVRENIIR 660

Qy         192 IEN 194
                ::
Db         661 YDD 663
```

RESULT 7
T13933
pol polyprotein - fruit fly (Drosophila virilis) retrotransposon Tv1 (fragment)
C;Species: Drosophila virilis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13933
R;Andrianov, B.V.; Zakharyev, V.M.; Evgen'ev, M.B.; Schuppe, N.G.
submitted to the EMBL Data Library, April 1998
A;Description: Gypsy group retrotransposon Tv1 from Drosophila virilis.
A;Reference number: Z17816
A;Accession: T13933
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1188 <AND>
A;Cross-references: UNIPROT:O76326; EMBL:AF056940; NID:g3493212; PID:g3493214; PIDN:AAC3
C;Genetics:
A;Gene: pol
A;Cross-references: FlyBase:FBgn0013099
A;Mobile element: retrotransposon Tv1
C;Superfamily: pol polyprotein

 Query Match 8.1%; Score 89.5; DB 2; Length 1188;
 Best Local Similarity 24.8%; Pred. No. 5.7;
 Matches 34; Conservative 27; Mismatches 41; Indels 35; Gaps 7;

```
Qy           5 LFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPNR 64
               | : :: ||||  :|        ||: | :   :   ||   ::|      ||  : |||
Db          81 LNYQISPIHAECTKPS-------RLTSRDSNSGQIRIWDNIGKFL------FSKPREPNR 127

Qy          65 EAT-------EISHVLLCNV----------TQRVSFWFVVTDPSKNHTLPAV-EVQSAIR 106
                  :       |::  | | :          | |::|  |  :  | ||:  | |:: :||
Db         128 NKSIHKNWIMELTKFLKCVIDTGSTINLMKTNRLNF-PVYNETLKVHTINGVIELKQSIR 186

Qy         107 MNKNRI---NNAFFLND 120
               :  ::|      |:::|
Db         187 LGASKICPSKQKFYIHD 203
```

RESULT 8
JC7294
alphaP integrin - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: JC7294
R;Susan, J.M.; Just, M.L.; Lennarz, W.J.
Biochem. Biophys. Res. Commun. 272, 929-935, 2000
A;Title: Cloning and characterization of alphaP integrin in embryos of the sea urchin St
A;Reference number: JC7294
A;Contents: Embryo
A;Accession: JC7294
A;Molecule type: mRNA
A;Residues: 1-1054 <SUS>
A;Cross-references: UNIPROT:Q9U6S1; GB:AAD55724
C;Genetics:
A;Gene: sualphaP
C;Superfamily: integrin alpha-2b chain
C;Keywords: calcium binding; embryo; glycolysis; glycoprotein; heterodimer; transmembran

 Query Match 8.1%; Score 89; DB 2; Length 1054;
 Best Local Similarity 20.5%; Pred. No. 5.5;
 Matches 56; Conservative 30; Mismatches 59; Indels 128; Gaps 13;

```
Qy          15 ELCQPGAENAFKVRLSIRTALGDKAYAW---DTNEEYLF---------------------- 50
               |:   |: || :| |:||          |    | | :|||
Db         795 EVRNTGSSNAAEVTLNIR---------WPEKDENGDYLFYLLGIMTDEGVTCQISQGQAN 845

Qy          51 ----------KAMVAFSMRKVPNRE-----------------ATEISHVLL-CNVTQ--- 79
                         |  :: |  :|  |                     |  | ||: | : :
Db         846 PLGVKLEASTKEQLSNSTTQVSGRRKREGEYAEALAQAEPIFCTPESCVLINCTIDEIKA 905

Qy          80 ------RV--SFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKIPST 131
                     |:   ||       : :  :| ::|  |                :  |    ||
Db         906 TKSKVVRILGRFWERTFQKAVSEAVPVIQVTLA-------------STATATVRSIPYN 951

Qy         132 LAPPMD-----------------PSVPI--WIIIFGVIFCIIIVAIALLILSGIWQ--- 168
               :  ||:                 | | |  |||:  |:  ||::   |:|: |:|:
Db         952 IPLPMEFTDSTKASTLITAEELVLPPVSIAWWIIVVSVLGGIILL---LIIILGLWKCGF 1008

Qy         169 -RRRKNKE---------------PSEVDDAEDK 185
                 |:|  |               | || || |:
Db        1009 FERKKPGEDQKEYEPVAVTEKDGPPEVYDAPDR 1041
```

RESULT 9
A37009
CD44 homolog membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 09-Jul-2004
C;Accession: A37009
R;Zhou, D.F.H.; Ding, J.F.; Picker, L.J.; Bargatze, R.F.; Butcher, E.C.; Goeddel, D.V.
J. Immunol. 143, 3390-3395, 1989
A;Title: Molecular cloning and expression of Pgp-1. The mouse homolog of the human H-CAM
A;Reference number: A37009; MUID:90038499; PMID:2681416
A;Accession: A37009

```
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <ZHO>
A;Cross-references: UNIPROT:P15379; GB:M30655; NID:g200332; PIDN:AAA39922.1; PID:g200333
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

  Query Match             8.0%;  Score 88;  DB 2;  Length 363;
  Best Local Similarity   21.6%;  Pred. No. 2;
  Matches   24;  Conservative   23;  Mismatches   30;  Indels   34;  Gaps    3;

Qy        128 IPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRR---------------- 171
              : :|  |   | :| |:||   :  :: :|: | :   :  |||
Db        256 VTTTSGPMRRPQIPEWLII---LASLLALALILAVCIAVNSRRRCGQKKKLVINGGNGTV 312

Qy        172 KNKEPSEVDDAEDKCENMITIENGIPSD--------------PLDMKGGI 207
              ::::|||::    | : |: : |  ||:               :||| |:
Db        313 EDRKPSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSVDMKIGV 363


RESULT 10
A34424
CD44 membrane glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 01-Dec-2000
C;Accession: A34424; A34907
R;Nottenburg, C.; Rees, G.; St. John, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989
A;Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate
A;Reference number: A34424; MUID:90046829; PMID:2682651
A;Accession: A34424
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-365 <NOT>
A;Cross-references: GB:M27130; NID:g192530; PIDN:AAA37407.1; PID:g309161
R;Wolffe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.
J. Biol. Chem. 265, 341-347, 1990
A;Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antige
A;Reference number: A34907; MUID:90094420; PMID:2403559
A;Accession: A34907
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 8-195,'G',197-365 <WOL>
A;Cross-references: GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:g200335
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

  Query Match             8.0%;  Score 88;  DB 2;  Length 365;
  Best Local Similarity   21.6%;  Pred. No. 2;
  Matches   24;  Conservative   23;  Mismatches   30;  Indels   34;  Gaps    3;

Qy        128 IPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRR---------------- 171
              : :|  |   | :| |:||   :  :: :|: | :   :  |||
Db        258 VTTTSGPMRRPQIPEWLII---LASLLALALILAVCIAVNSRRRCGQKKKLVINGGNGTV 314

Qy        172 KNKEPSEVDDAEDKCENMITIENGIPSD--------------PLDMKGGI 207
              ::::|||::    | : |: : |  ||:               :||| |:
Db        315 EDRKPSELNGEASKSQEMVHLVNKEPSETPDQCMTADETRNLQSVDMKIGV 365


RESULT 11
A35616
T-cell surface glycoprotein CD44 - hamster
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: A35616
R;Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed, B.
Cell 61, 1303-1313, 1990
A;Title: CD44 is the principal cell surface receptor for hyaluronate.
A;Reference number: A35616; MUID:90304889; PMID:1694723
A;Accession: A35616
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-362 <ARU>
A;Cross-references: UNIPROT:P20944
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; transmembrane protein

  Query Match             7.8%;  Score 86;  DB 2;  Length 362;
  Best Local Similarity   22.0%;  Pred. No. 3;
  Matches   24;  Conservative   22;  Mismatches   29;  Indels   34;  Gaps    3;

Qy        130 STLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRR----------------KN 173
              :|  |   | :| |:|   |:  :: :|: | :   :  |||                ::
Db        257 TTSRPGRKPQIPEWLI---VLASLLALALILAVCIAVNSRRRCGQKKKLVINSGNGKVED 313

Qy        174 KEPSEVDDAEDKCENMITIENGIPSDP--------------LDMKGGI 207
              ::|||::    | : |: : |  ||:                :||| |:
Db        314 RKPSELNGEASKSQEMVHLVNKEPSETPDQFMTADETRNLQNVDMKIGV 362


RESULT 12
B38745
cell adhesion molecule CD44 precursor, long form (meta-1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: B38745; A38745
R;Guenthert, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; HauBmann, I.; Matzku, S.,
Cell 65, 13-24, 1991
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to rat carcinoma
A;Reference number: A38745; MUID:91191552; PMID:1707342
A;Accession: B38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-503 <GUE>
A;Cross-references: UNIPROT:P26051; GB:M61874; NID:g576534; PIDN:AAA53534.1; PID:g576535
A;Accession: A38745
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-223,386-503 <GU2>
A;Cross-references: GB:M61875
C;Keywords: cell adhesion

  Query Match             7.8%;  Score 86;  DB 2;  Length 503;
  Best Local Similarity   20.7%;  Pred. No. 4.4;
  Matches   23;  Conservative   24;  Mismatches   30;  Indels   34;  Gaps    3;

Qy        128 IPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRR---------------- 171
              : :|  |   | :| |:||   :  :: :|: | :   :  |||
Db        396 VTTTSGPARRPQIPEWLII---LASLLALALILAVCIAVNSRRRCGQKKKLVINSGNGTV 452

Qy        172 KNKEPSEVDDAEDKCENMITIENGIPSD--------------PLDMKGGI 207
              ::::|||::    | : |: : |  ||:               :||| |:
Db        453 EDRKPSELNGEASKSQEMVHLVNKEPTETPDQFMTADETRNLQSVDMKIGV 503


RESULT 13
T47482
receptor-like protein kinase - Arabidopsis thaliana
N;Alternate names: protein F18N11.180
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Aug-2004
C;Accession: T47482
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24467
A;Accession: T47482
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-667 <JOR>
A;Cross-references: UNIPROT:Q9M3D7; EMBL:AL132953
A;Experimental source: cultivar Columbia; BAC clone F18N11
C;Genetics:
A;Map position: 3
A;Note: F18N11.180
C;Superfamily: protein kinase homology
```

```
  Query Match             7.8%;  Score 85.5;  DB 2;  Length 667;
  Best Local Similarity   21.6%;  Pred. No. 6.8;
  Matches   37;  Conservative   23;  Mismatches   64;  Indels   47;  Gaps    6;

Qy         81 VSFWFVVTDPSKNHTLPAVEVQSAIR----------------------MNKNRINNAFF 117
              |  |         | ||  :|:|   |                      |    :| :
Db        192 VQVWIDYDGSLLNVTLAPIEIQKPNRPLISRDINLSEIFQDKMYIGFSGSNGRLTSNQYI 251

Qy        118 LN---------DQTLEFLKIPSTLAP-------PMDPSVPIWIIIFGVIFCIIIVAIALL 161
              |           |:|:  |:|     |       | :    :  :: |::  |::|   |:
Db        252 LGWSFSKSKEFMQSLDLSKLPQAPIPRNEQAPVPREEKKKLHPLLIGLV--ILLVIPVLM 309

Qy        162 ILSGI-WQRRRKNKEPSEVDDAE-----DKCENMITIENGIPSDPLDMKGG 206
              :| |: | ||:|  |  |  : |       :::    ||   | |  |||
Db        310 VLGGVYWYRRKKYAEVKESWEKEYGPHRYSYKSLYKATNGFVKDALVGKGG 360


RESULT 14
E81924
probable two-component system sensor kinase (EC 2.7.3.-) NMA0797 [imported] - Neisseria
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: E81924
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81924
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-468 <PAR>
A;Cross-references: UNIPROT:Q9JVK7; GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB8408
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA0797
C;Keywords: phosphotransferase

  Query Match             7.7%;  Score 84.5;  DB 2;  Length 468;
  Best Local Similarity   23.7%;  Pred. No. 5.5;
  Matches   47;  Conservative   29;  Mismatches   81;  Indels   41;  Gaps    9;

Qy         21 AENAFKVRLSIRTAL----------GDKAYAWDTNEEYLFKAMVAFSMRKVPNREATEI 69
              ||| |  | :| | |          || | | :   |:   : |:  :  :   |  :|
Db         34 AENQFNQRRTIETTLMGSIISAFRARGD-AGAREILTEWK-DSPVSSGVYVIQGDEKKDI 91

Qy         70 SHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINN--AFFLND-QTLEFL 126
                |  : : |   :  |    |  |           : :  :|      ||  |   |:
Db         92 LHRYIDSYTIERARLFAAGHPHSN----------LVHIEYDRFGEEYLFFTKDWDKLQAR 141

Qy        127 KIPSTLAPPMDPSVPIW--------IIIFGVIFCIII---VAIALLILSGIWQR----RR 171
              ::||  |   |  |||         ||| |::   |:   :|  : ||     |
Db        142 RLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAGNIAKPIRILGNGMDRVANGEL 201

Qy        172 KNKEPSEVDDAEDKCENM 189
              : :   :||| :|:  ::
Db        202 ETRISQQVDDRDDELSHL 219


RESULT 15
JG0022
flagellar basal-body M-ring protein fliF - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C;Accession: JG0022; A42365; B69624; S14494
R;Zuberi, A.R.; Ying, C.; Bischoff, D.S.; Ordal, G.W.
Gene 101, 23-31, 1991
A;Title: Gene-protein relationships in the flagellar hook-basal body complex of Bacillus
A;Reference number: JG0019; MUID:91285431; PMID:1905667
A;Accession: JG0022
A;Molecule type: DNA
A;Residues: 1-536 <ZUB>
A;Cross-references: UNIPROT:P23447; GB:M54965
R;Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A;Title: The flaA locus of Bacillus subtilis is part of a large operon coding for flagel
A;Reference number: A42365; MUID:91258343; PMID:1828465
A;Accession: A42365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 355-536 <ALB>
A;Cross-references: GB:M72718; EMBL:X56049; NID:g39904; PIDN:CAA39520.1; PID:g3979709
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69624
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-536 <KUN>
A;Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13494.1; PID:e1185212;
A;Experimental source: strain 168
C;Genetics:
A;Gene: fliF

  Query Match             7.7%;  Score 84.5;  DB 2;  Length 536;
  Best Local Similarity   19.9%;  Pred. No. 6.5;
  Matches   39;  Conservative   36;  Mismatches   68;  Indels   53;  Gaps    8;

Qy          9 VTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVPNREATE 68
              |  || |:    ||: :|||               |   : : :   | :   :     :
Db        352 VNRIHKEI----AESPYKVR-------------DLGIQVMVEPPDAKNTASLSTERQDD 393

Qy         69 ISHVLLCNVTQRVSFWFVVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLEFLKI 128
              |  :|  :  | |   :  | ::|  |   :: : | ::    :   |:  | |
Db        394 IQKIL--STVVRTS---LDKDETQNQNLSDADINNKIVVSVQPFDGKVNLDTNTEE---- 444

Qy        129 PSTLAPPMDPSVPIW-IIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKCE 187
                        :|:|  |: ||:   ||| | :||       |:|  :  | :: | :
Db        445 --------SSGIPLWAYIVGGVLIAAIIVLIIMLI-------RKKRAQEDEFEEYEYE-- 487

Qy        188 NMITIENGIPSDPLDM 203
                    :| :|:::
Db        488 --------VPQEPINL 495


Search completed: August 18, 2005, 17:34:15
Job time : 42 secs
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GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: August 18, 2005, 17:27:03 ; Search time 72 Seconds
(without alignments)
1138.794 Million cell updates/sec

Title: US-09-997-641-387
Perfect score: 1102
Sequence: 1 MLWLLFFLVTAIHAELCQPG.....ENGIPSDPLDMKGGILMMPS 212
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description

RESULT 1
ID AAY66751 standard; protein; 212 AA.
DE Membrane-bound protein PRO1312.
PN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 2
ID AAB33447 standard; protein; 212 AA.
DE Human PRO1312 protein UNQ678 SEQ ID NO:161.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 3
ID AAB24430 standard; protein; 212 AA.
DE Human PRO1312 protein sequence SEQ ID NO:214.
PN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 4
ID AAU12412 standard; protein; 212 AA.
DE Human PRO1312 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 5
ID AAB65274 standard; protein; 212 AA.
DE Human PRO1312 (UNQ678) protein sequence SEQ ID NO:387.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 6
ID ABU58089 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 7
ID ABU59167 standard; protein; 212 AA.
DE Novel human secreted or transmembrane protein PRO1312.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 8
ID ABU82679 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 9
ID ABO17856 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 10
ID ABU60598 standard; protein; 212 AA.
DE Human secreted/transmembrane protein, #157.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 11
ID ABU13980 standard; protein; 212 AA.
DE Human PRO1312 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 12
ID ABU81110 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 13
ID ABU72565 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 14
ID ABU66810 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 15
ID ABU59891 standard; protein; 212 AA.
DE Novel secreted and transmembrane protein PRO1312.
PN US2003017563-A1.
PD 23-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 16
ID ABU59314 standard; protein; 212 AA.
DE Human secreted/transmembrane protein, #157.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 17
ID ABO26011 standard; protein; 212 AA.
DE Human PRO1312 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 18
ID ABO25081 standard; protein; 212 AA.
DE Human secreted/transmembrane protein (PRO) #241.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 19
ID ABU59020 standard; protein; 212 AA.
DE Human sectreted/transmembrane protein, #157.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 20
ID ABU92398 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 21
ID ABU59463 standard; protein; 212 AA.
DE Novel human secreted or transmembrane protein PRO1192.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 22
ID ABU67086 standard; protein; 212 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 482.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 23
ID ABU92229 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 24
ID ABU10935 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 25
ID ABU81687 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 26
ID ABU88626 standard; protein; 212 AA.
DE Human secreted and transmembrane polypeptide PRO1312.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 27
ID ABO34140 standard; protein; 212 AA.
DE Human PRO1312 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 28
ID ADA46001 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 29
ID ADA76432 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 30
ID ADA19082 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 31
ID ADA61705 standard; protein; 212 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 32
ID ADB19490 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 33
ID ADB28031 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 34
ID ADA86510 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082711-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 35
ID ADB16074 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 36
ID ADA37898 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 37
ID ADA47860 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 38
ID ADA21584 standard; protein; 212 AA.
DE Human secreted/transmembrane polypeptide PRO1312.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 39
ID ADA10371 standard; protein; 212 AA.
DE Human secreted/transmembrane protein, PRO1312.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 40
ID ADA67655 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 41
ID ADB30662 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 42
ID ADA85958 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 43
ID ADA17915 standard; protein; 212 AA.
DE Human PRO1312 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 44
ID ADA97170 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 45
ID ADA79474 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 46
ID ADA87613 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 47
ID ADB16815 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 48
ID ADA28023 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 49
ID ADA91907 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 50
ID ADB14970 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 51
ID ADB18931 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 52
ID ADA94146 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 53
ID ADB20042 standard; protein; 212 AA.

DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 54
ID ADB13354 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 55
ID ABO43389 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 56
ID ADA94603 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 57
ID ADA74608 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 58
ID ADB24841 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 59
ID ADA82365 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 60
ID ADA75328 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 61
ID ADA85406 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 62
ID ADA84854 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 63
ID ADB30110 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 64
ID ADA80638 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 65
ID ADA75880 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 66
ID ADA38828 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 67
ID ADA47105 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 68
ID ADB25401 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 69
ID ADA93577 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 70
ID ADB26927 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 71
ID ADB31214 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 72
ID ADA92949 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 73
ID ADA61142 standard; protein; 212 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 74
ID ADB24289 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 75
ID ADA96618 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 76
ID ADA81190 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 77
ID ADA96066 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 78
ID ADB26375 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 79
ID ADB21860 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 80
ID ADA77639 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 81
ID ADB18379 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 82
ID ADA87062 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 83
ID ADA88165 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 84
ID ADA46553 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 85
ID ADB28583 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 86
ID ADB29135 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 87
ID ABO53226 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 88
ID ADA77087 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 89
ID ADA22510 standard; protein; 212 AA.
DE Human secreted/transmembrane polypeptide PRO1312.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 90
ID ADA88717 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.

PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 91
ID ADA97722 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 92
ID ADB27479 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 93
ID ADB22412 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 94
ID ABO22596 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 95
ID ADA06676 standard; protein; 212 AA.
DE Human secreted/transmembrane PRO polypeptide #121.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 96
ID ADA39369 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 97
ID ADA67103 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 98
ID ADB22964 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 99
ID ADB23737 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 100
ID ADA92459 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 101
ID ADB15522 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 102
ID ADB38774 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 103
ID ADB96395 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 104
ID ADB38222 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 105
ID ADB66694 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 106
ID ADB89774 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 107
ID ADB90506 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 108
ID ADB39607 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 109
ID ADB47230 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.

PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 110
ID ADB86837 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 111
ID ADB77442 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 112
ID ADB34599 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 113
ID ADB35703 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 114
ID ADB34047 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 115
ID ADB35151 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 116
ID ADB36255 standard; protein; 212 AA.
DE Human PRO polypeptide SEQ ID NO 482.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 117
ID ADB46650 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 118
ID ADC57867 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 119
ID ADC55231 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 120
ID ADC12098 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 121
ID ADC56520 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 122
ID ADC07575 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 123
ID ADC11565 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 124
ID ADC50523 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 125
ID ADC72070 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 126
ID ADC60049 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 127
ID ADC53056 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 128
ID ADC57410 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.

PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 129
ID ADC60601 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 130
ID ADC51076 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 131
ID ADC65603 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 132
ID ADC54701 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 133
ID ADC53662 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 134
ID ADC59185 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 135
ID ADC56063 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 136
ID ADC58633 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein Seq ID482.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 137
ID ADC14687 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 138
ID ADD08219 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 139
ID ADD03307 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 140
ID ADC90299 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 141
ID ADC82044 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 142
ID ADC69718 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 143
ID ADC48607 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 144
ID ADD10136 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 145
ID ADD07686 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 146
ID ADD04711 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;

RESULT 147
ID ADC82577 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003059833-A1.
PD 27-MAR-2003..
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 148
ID ADC80667 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 149
ID ADD11174 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 150
ID ADC48055 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 151
ID ADD08757 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 152
ID ADC80115 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 153
ID ADD07006 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 154
ID ADD09584 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 155
ID ADC83253 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 156
ID ADD41297 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 157
ID ADD52436 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 158
ID ADD53176 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 159
ID ADD53728 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 160
ID ADD55360 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 161
ID ADD56318 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 162
ID ADD51884 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 163
ID ADD02683 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 164
ID ADD02117 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 165
ID ADD54299 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;

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  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 166
ID   ADD54756 standard; protein; 212 AA.
DE   Human PRO polypeptide #121.
PN   US2002132253-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 167
ID   ADD92616 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003199030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 168
ID   ADD91512 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003199055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 169
ID   ADE04126 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003199057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 170
ID   ADE26910 standard; protein; 212 AA.
DE   Novel human secreted and transmembrane protein PRO1312.
PN   US2003087304-A1.
PD   08-MAY-2003.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 171
ID   ADE32423 standard; protein; 212 AA.
DE   Novel human secreted and transmembrane protein PRO1312.
PN   US2003194765-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 172
ID   ADE22355 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003199056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 173
ID   ADD79579 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003203428-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 174
ID   ADE42115 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003194772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 175
ID   ADE17932 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003199023-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 176
ID   ADD92064 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003199053-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 177
ID   ADE33527 standard; protein; 212 AA.
DE   Novel human secreted and transmembrane protein PRO1312.
PN   US2003194767-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 178
ID   ADE34079 standard; protein; 212 AA.
DE   Novel human secreted and transmembrane protein PRO1312.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 179
ID   ADD80131 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003207417-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 180
ID   ADD93168 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003194768-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 181
ID   ADE19588 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003199025-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 182
ID   ADE19036 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003199026-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 183
ID   ADE43232 standard; protein; 212 AA.
DE   Human PRO polypeptide #241.
PN   US2003199033-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             100.0%;  Score 1102;  DB 7;  Length 212;
  Best Local Similarity   100.0%;  Pred. No. 8e-114;
RESULT 184
ID   ADD96021 standard; protein; 212 AA.
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DE Human PRO polypeptide #241.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 185
ID ADE22907 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 186
ID ADD79025 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 187
ID ADE26377 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 188
ID ADE32975 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 189
ID ADE42667 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 190
ID ADD80683 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 191
ID ADD89711 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 192
ID ADE40995 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 193
ID ADE04794 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 194
ID ADE92923 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 195
ID ADF67314 standard; protein; 212 AA.
DE Human PRO1312 amino acid sequence SEQ ID NO:387.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 196
ID ADG21632 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 197
ID ADG23273 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 198
ID ADF97608 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 199
ID ADG80672 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 200
ID ADG80120 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 201
ID ADH55412 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 202
ID ADH55964 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207379-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 203
ID ADI35568 standard; protein; 212 AA.
DE Human PRO polypeptide #121.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 204
ID ADI64183 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 205
ID ADI65132 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 206
ID ADI63631 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 207
ID ADH82045 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 208
ID ADI00061 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 209
ID ADH81493 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 210
ID ADM82662 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 211
ID ADN16061 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 212
ID ADN16690 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 213
ID ADN15509 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 214
ID ADN14957 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 7; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 215
ID ADC81219 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 216
ID ADD76667 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 217
ID ADD88031 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 218
ID ADD86435 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 219
ID ADE75883 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 220
ID ADE23459 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 221

ID ADE24011 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 222
ID ADE24654 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 223
ID ADD87479 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 224
ID ADE89345 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 225
ID ADE18484 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 226
ID ADE88793 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 227
ID ADE94813 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 228
ID ADE91224 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 229
ID ADF35513 standard; protein; 212 AA.
DE Human PRO1312 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 230
ID ADE95365 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 231
ID ADE93475 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 232
ID ADF35056 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 233
ID ADE92371 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 234
ID ADE90672 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 235
ID ADE91819 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 236
ID ADG11763 standard; protein; 212 AA.
DE Human PRO1312 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 237
ID ADG02398 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 238
ID ADG22184 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 239
ID ADG20254 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207376-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 240
ID ADF98160 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 241
ID ADG24377 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 242
ID ADF98731 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 243
ID ADG03562 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 244
ID ADF99283 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 245
ID ADG16868 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 246
ID ADG05327 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 247
ID ADG19594 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 248
ID ADG13431 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 249
ID ADG08488 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 250
ID ADG15658 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 251
ID ADF97056 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 252
ID ADG06241 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 253
ID ADG23825 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 254
ID ADG04114 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 255
ID ADG25015 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 256
ID ADG07312 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 257
ID ADG07864 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 258
ID ADG55359 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 259
ID ADG61023 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 260
ID ADG62127 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 261
ID ADG82328 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 262
ID ADG57567 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 263
ID ADG57015 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 264
ID ADG55911 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 265
ID ADG58671 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 266
ID ADG71037 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 267
ID ADG58119 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 268
ID ADG53703 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 269
ID ADG71589 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 270
ID ADG81776 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 271
ID ADH19633 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 272
ID ADH30738 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 273
ID ADH12105 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 274
ID ADG52527 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 275
ID ADG54255 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 276

ID ADG81224 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 277
ID ADG56463 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 278
ID ADH12729 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 279
ID ADH21126 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 280
ID ADG61575 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 281
ID ADH20166 standard; protein; 212 AA.
DE Human secreted/transmembrane protein PRO1312.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 282
ID ADH28662 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 283
ID ADG54807 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 284
ID ADG59847 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 285
ID ADI81271 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 286
ID ADG10014 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 287
ID ADI15485 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 288
ID ADG09362 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 289
ID ADI14817 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 290
ID ADI18412 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 291
ID ADJ63693 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 292
ID ADJ77588 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 293
ID ADJ65710 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 294
ID ADM27846 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2004048333-A1.

PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 295
ID ADM42570 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 296
ID ADM28432 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 297
ID ADI95914 standard; protein; 212 AA.
DE Human PRO polypeptide #241.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 298
ID ADI96466 standard; protein; 212 AA.
DE Novel human secreted and transmembrane protein PRO1312.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 299
ID ADT94384 standard; protein; 212 AA.
DE Human PRO1312 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1102; DB 8; Length 212;
Best Local Similarity 100.0%; Pred. No. 8e-114;
RESULT 300
ID AAB88580 standard; protein; 222 AA.
DE Human hydrophobic domain containing protein clone HP10720 #64.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 97.4%; Score 1073; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e-110;
RESULT 301
ID ADA56986 standard; protein; 222 AA.
DE Human secreted protein #269.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.4%; Score 1073; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e-110;
RESULT 302
ID ADA40837 standard; protein; 222 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.4%; Score 1073; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e-110;
RESULT 303
ID ABR01796 standard; protein; 222 AA.
DE Human cancer-related protein, 156P1D4.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 97.4%; Score 1073; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e-110;
RESULT 304
ID ADA11613 standard; protein; 222 AA.
DE Human novel secreted protein, SEQ ID NO 141.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.4%; Score 1073; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e-110;
RESULT 305
ID ADD37902 standard; protein; 222 AA.
DE Human secreted protein #85.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.4%; Score 1073; DB 7; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e-110;
RESULT 306
ID AAW29670 standard; protein; 222 AA.
DE Homo sapiens clone AM42_3 secreted protein.
PN WO9832853-A2.
PD 30-JUL-1998.
PA (GEMY) GENETICS INST INC.
Query Match 97.1%; Score 1070; DB 2; Length 222;
Best Local Similarity 99.5%; Pred. No. 3.1e-110;
RESULT 307
ID ADE11757 standard; protein; 222 AA.
DE Human secreted polypeptide #12.
PN US2003100051-A1.
PD 29-MAY-2003.
PA (RUBE/) RUBEN S M.
PA (FLOR/) FLORENCE K A.
PA (NIJJ/) NI J.
PA (ROSE/) ROSEN C A.
PA (CART/) CARTER K C.
PA (MOOR/) MOORE P A.
PA (OLSE/) OLSEN H S.
PA (SHIY/) SHI Y.
PA (YOUN/) YOUNG P E.
PA (WEIY/) WEI Y.
PA (BREW/) BREWER L A.
PA (SOPP/) SOPPET D R.
PA (LAFL/) LAFLEUR D W.
PA (ENDR/) ENDRESS G A.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 96.7%; Score 1066; DB 7; Length 222;
Best Local Similarity 99.5%; Pred. No. 8.7e-110;
RESULT 308
ID AAY76135 standard; protein; 223 AA.
DE Human secreted protein encoded by gene 12.
PN WO9958660-A1.
PD 18-NOV-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.7%; Score 1066; DB 3; Length 223;
Best Local Similarity 99.5%; Pred. No. 8.7e-110;
RESULT 309
ID AAY04156 standard; protein; 222 AA.
DE Human 5' EST secreted protein SEQ ID NO:27.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 95.1%; Score 1048; DB 2; Length 222;
Best Local Similarity 98.1%; Pred. No. 8.7e-108;
RESULT 310
ID AAW93620 standard; protein; 222 AA.
DE Human 5' EST secreted protein clone 58-35-2-F1O-FL2.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.

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  Query Match             95.1%;  Score 1048;  DB 2;  Length 222;
  Best Local Similarity   98.1%;  Pred. No. 8.7e-108;
RESULT 311
ID   AAY35890 standard; protein; 222 AA.
DE   Extended human secreted protein sequence, SEQ ID NO. 27.
PN   WO9931236-A2.
PD   24-JUN-1999.
PA   (GEST ) GENSET.
  Query Match             95.1%;  Score 1048;  DB 2;  Length 222;
  Best Local Similarity   98.1%;  Pred. No. 8.7e-108;
RESULT 312
ID   AAY59653 standard; protein; 222 AA.
DE   Secreted protein extended EST protein sequence #6.
PN   WO9940189-A2.
PD   12-AUG-1999.
PA   (GEST ) GENSET.
  Query Match             95.1%;  Score 1048;  DB 2;  Length 222;
  Best Local Similarity   98.1%;  Pred. No. 8.7e-108;
RESULT 313
ID   AAY01594 standard; protein; 222 AA.
DE   Secreted protein encoded by an extended 5' EST cDNA sequence.
PN   WO9906554-A2.
PD   11-FEB-1999.
PA   (GEST ) GENSET.
  Query Match             95.1%;  Score 1048;  DB 2;  Length 222;
  Best Local Similarity   98.1%;  Pred. No. 8.7e-108;
RESULT 314
ID   AAY12986 standard; protein; 222 AA.
DE   Human secreted protein encoded by 5' EST clone 58-35-2-F10-FL2.
PN   WO9906552-A2.
PD   11-FEB-1999.
PA   (GEST ) GENSET.
  Query Match             95.1%;  Score 1048;  DB 2;  Length 222;
  Best Local Similarity   98.1%;  Pred. No. 8.7e-108;
RESULT 315
ID   AAY25459 standard; protein; 222 AA.
DE   Human secreted protein 6 derived from extended cDNA.
PN   WO9925825-A2.
PD   27-MAY-1999.
PA   (GEST ) GENSET.
  Query Match             95.1%;  Score 1048;  DB 2;  Length 222;
  Best Local Similarity   98.1%;  Pred. No. 8.7e-108;
RESULT 316
ID   AAY12680 standard; peptide; 222 AA.
DE   Human 5' EST secreted protein.
PN   WO9906549-A2.
PD   11-FEB-1999.
PA   (GEST ) GENSET.
  Query Match             95.1%;  Score 1048;  DB 2;  Length 222;
  Best Local Similarity   98.1%;  Pred. No. 8.7e-108;
RESULT 317
ID   AAG00014 standard; protein; 222 AA.
DE   Human secreted protein #3.
PN   EP1033401-A2.
PD   06-SEP-2000.
PA   (GEST ) GENSET.
  Query Match             95.1%;  Score 1048;  DB 3;  Length 222;
  Best Local Similarity   98.1%;  Pred. No. 8.7e-108;
RESULT 318
ID   AAY04174 standard; protein; 222 AA.
DE   Human 5' EST secreted protein SEQ ID NO:27.
PN   WO9906548-A2.
PD   11-FEB-1999.
PA   (GEST ) GENSET.
  Query Match             94.4%;  Score 1040;  DB 2;  Length 222;
  Best Local Similarity   97.6%;  Pred. No. 6.8e-107;
RESULT 319
ID   AAM23565 standard; protein; 184 AA.
DE   Human EST encoded protein SEQ ID NO: 1090.
PN   WO200154477-A2.
PD   02-AUG-2001.
PA   (HYSE-) HYSEQ INC.
  Query Match             86.1%;  Score 949;  DB 4;  Length 184;
  Best Local Similarity   99.5%;  Pred. No. 6.9e-97;
RESULT 320
ID   ADO07065 standard; protein; 217 AA.
DE   Human protein modification and maintenance molecule 26 (PMMM-26).
PN   WO2004033636-A2.
PD   22-APR-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             80.3%;  Score 885;  DB 8;  Length 217;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-89;
RESULT 321
ID   AAY11999 standard; protein; 136 AA.
DE   Human 5' EST secreted protein SEQ ID NO: 312.
PN   WO9906554-A2.
PD   11-FEB-1999.
PA   (GEST ) GENSET.
  Query Match             63.0%;  Score 694;  DB 2;  Length 136;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-68;
RESULT 322
ID   AAY36576 standard; protein; 176 AA.
DE   Fragment of human secreted protein encoded by gene 42.
PN   WO9931117-A1.
PD   24-JUN-1999.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             60.2%;  Score 663;  DB 2;  Length 176;
  Best Local Similarity   96.3%;  Pred. No. 4.3e-65;
RESULT 323
ID   ADA11746 standard; protein; 176 AA.
DE   Human novel secreted protein associated polypeptide #16.
PN   US2003055236-A1.
PD   20-MAR-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             60.2%;  Score 663;  DB 6;  Length 176;
  Best Local Similarity   96.3%;  Pred. No. 4.3e-65;
RESULT 324
ID   ADN42960 standard; protein; 119 AA.
DE   Human secreted protein SECP-21.
PN   WO2004037987-A2.
PD   06-MAY-2004.
PA   (INCY-) INCYTE CORP.
  Query Match             43.5%;  Score 479.5;  DB 8;  Length 119;
  Best Local Similarity   50.0%;  Pred. No. 6.4e-45;
RESULT 325
ID   ADA57438 standard; protein; 104 AA.
DE   Human secreted protein #269.
PN   WO2002102994-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             37.7%;  Score 415;  DB 6;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 8e-38;
RESULT 326
ID   ADA41317 standard; protein; 104 AA.
DE   Human secreted protein.
PN   WO2002102993-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             37.7%;  Score 415;  DB 6;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 8e-38;
RESULT 327
ID   ADD38041 standard; protein; 104 AA.
DE   Human secreted protein #224.
PN   WO200290526-A2.
PD   14-NOV-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             37.7%;  Score 415;  DB 7;  Length 104;
  Best Local Similarity   100.0%;  Pred. No. 8e-38;
RESULT 328
ID   AAY36265 standard; protein; 105 AA.
DE   Human secreted protein encoded by gene 42.
PN   WO9931117-A1.
PD   24-JUN-1999.
PA   (HUMA-) HUMAN GENOME SCI INC.
  Query Match             37.7%;  Score 415;  DB 2;  Length 105;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-38;
```

RESULT 329
ID ADA11718 standard; protein; 105 AA.
DE Human novel secreted protein, SEQ ID NO 246.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 37.7%; Score 415; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.1e-38;
RESULT 330
ID ABM85140 standard; protein; 768 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5389.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 34.1%; Score 376; DB 8; Length 768;
Best Local Similarity 47.9%; Pred. No. 2.8e-32;
RESULT 331
ID AAY84562 standard; protein; 805 AA.
DE A human angiotensin converting enzyme-2 (ACE-2) protein.
PN WO200018899-A2.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 3; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 332
ID AAY67310 standard; protein; 805 AA.
DE Human MPROT15 amino acid sequence #1.
PN JP11318472-A.
PD 24-NOV-1999.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 34.1%; Score 376; DB 3; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 333
ID AAB48095 standard; protein; 805 AA.
DE Human Zace2 protein.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 334
ID AAY72667 standard; protein; 805 AA.
DE Human angiotensin converting enzyme-2 (ACE-2).
PN US6194556-B1.
PD 27-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 4; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 335
ID AAE20353 standard; protein; 805 AA.
DE Human ACE-2 full-length protein.
PN WO200212471-A2.
PD 14-FEB-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 5; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 336
ID ABG77011 standard; protein; 805 AA.
DE Human angiotensin converting enzyme 2.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match 34.1%; Score 376; DB 5; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 337
ID ABG77023 standard; protein; 805 AA.
DE Human angiotensin converting enzyme 2 variant #1.
PN WO200261131-A2.
PD 08-AUG-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (TSUC/) TSUCHIHASHI Z.
PA (HUIL/) HUI L.
Query Match 34.1%; Score 376; DB 5; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 338
ID AAU99701 standard; protein; 805 AA.
DE Human angiotensin converting enzyme-2 (ACE-2) protein.
PN WO200239997-A2.
PD 23-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 5; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 339
ID ABU07731 standard; protein; 805 AA.
DE Human zinc metallopeptidase Zace2.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 34.1%; Score 376; DB 6; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 340
ID ADA03344 standard; protein; 805 AA.
DE Human angiotensin converting enzyme 2-like protein.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.1%; Score 376; DB 6; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 341
ID ABR56712 standard; protein; 805 AA.
DE Human ACE-2 protein SEQ ID NO:142.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 34.1%; Score 376; DB 6; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 342
ID ADC38728 standard; protein; 805 AA.
DE Human secreted protein #41.
PN US2002193567-A1.
PD 19-DEC-2002.
PA (GEMY) GENETICS INST INC.
Query Match 34.1%; Score 376; DB 7; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 343
ID ADL95395 standard; protein; 805 AA.
DE Human angiotensin converting enzyme-2 (ACE-2).
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 7; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 344
ID ADL95494 standard; protein; 805 AA.
DE Human angiotensin converting enzyme-2 (ACE-2) N720D.
PN US6610497-B1.
PD 26-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 34.1%; Score 376; DB 7; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 345
ID ADH51357 standard; protein; 805 AA.
DE Human angiotensin-converting enzyme homologue ACE2.
PN WO2004000367-A1.
PD 31-DEC-2003.
PA (UYHE-) UNIV HEALTH NETWORK.
Query Match 34.1%; Score 376; DB 8; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 346
ID ADO55144 standard; protein; 805 AA.
DE Protein #46 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.

Query Match 34.1%; Score 376; DB 8; Length 805;
Best Local Similarity 47.9%; Pred. No. 3e-32;
RESULT 347
ID ADA03340 standard; protein; 711 AA.
DE Human angiotensin converting enzyme 2 protein.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 362; DB 6; Length 711;
Best Local Similarity 48.8%; Pred. No. 9.2e-31;
RESULT 348
ID AAB48097 standard; protein; 805 AA.
DE Mouse Zace2-5 protein.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 32.8%; Score 361; DB 4; Length 805;
Best Local Similarity 40.9%; Pred. No. 1.4e-30;
RESULT 349
ID AAB48098 standard; protein; 805 AA.
DE Mouse Zace2-10 protein.
PN WO200070032-A1.
PD 23-NOV-2000.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 32.8%; Score 361; DB 4; Length 805;
Best Local Similarity 40.9%; Pred. No. 1.4e-30;
RESULT 350
ID ABU07733 standard; protein; 805 AA.
DE Mouse zinc metallopeptidase mZace-5.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 32.8%; Score 361; DB 6; Length 805;
Best Local Similarity 40.9%; Pred. No. 1.4e-30;
RESULT 351
ID ABU07734 standard; protein; 805 AA.
DE Mouse zinc metallopeptidase mZace-10.
PN US2002177211-A1.
PD 28-NOV-2002.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 32.8%; Score 361; DB 6; Length 805;
Best Local Similarity 40.9%; Pred. No. 1.4e-30;
RESULT 352
ID AAU09092 standard; protein; 711 AA.
DE Novel human protein NHP #1.
PN WO200174896-A1.
PD 11-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.6%; Score 359; DB 4; Length 711;
Best Local Similarity 47.2%; Pred. No. 2e-30;
RESULT 353
ID ABR56709 standard; protein; 711 AA.
DE Human ACE-2 protein SEQ ID NO:138.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.6%; Score 359; DB 6; Length 711;
Best Local Similarity 47.2%; Pred. No. 2e-30;
RESULT 354
ID ABB40295 standard; peptide; 64 AA.
DE Peptide #7801 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.9%; Score 330; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;
RESULT 355
ID AAM33978 standard; protein; 64 AA.
DE Peptide #8015 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.9%; Score 330; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;
RESULT 356
ID ABB24701 standard; protein; 64 AA.
DE Protein #6700 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.9%; Score 330; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;
RESULT 357
ID AAM73792 standard; protein; 64 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34098.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.9%; Score 330; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;
RESULT 358
ID AAM61088 standard; protein; 64 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 33193.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.9%; Score 330; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;
RESULT 359
ID ABG55539 standard; peptide; 64 AA.
DE Human liver peptide, SEQ ID No 34187.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.9%; Score 330; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;
RESULT 360
ID ABG43678 standard; peptide; 64 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 33343.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 29.9%; Score 330; DB 5; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.2e-28;
RESULT 361
ID ABM85139 standard; protein; 771 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5388.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 27.0%; Score 297; DB 8; Length 771;
Best Local Similarity 41.2%; Pred. No. 1.8e-23;
RESULT 362
ID ADA03342 standard; protein; 681 AA.
DE Human angiotensin converting enzyme 2 extracellular domain.
PN WO200298448-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.2%; Score 289; DB 6; Length 681;
Best Local Similarity 48.1%; Pred. No. 1.1e-22;
RESULT 363
ID ABR56711 standard; protein; 681 AA.
DE Human ACE-2 extracellular domain SEQ ID NO:140.
PN WO200298906-A1.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.2%; Score 289; DB 6; Length 681;
Best Local Similarity 48.1%; Pred. No. 1.1e-22;
RESULT 364
ID AAY36579 standard; protein; 24 AA.
DE Fragment of human secreted protein encoded by gene 42.
PN WO9931117-A1.
PD 24-JUN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.1%; Score 133; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;

RESULT 365
ID ADA11749 standard; protein; 24 AA.
DE Human novel secreted protein associated polypeptide #19.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.1%; Score 133; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
RESULT 366
ID AAY36578 standard; protein; 23 AA.
DE Fragment of human secreted protein encoded by gene 42.
PN WO9931117-A1.
PD 24-JUN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 117; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
RESULT 367
ID ADA11748 standard; protein; 23 AA.
DE Human novel secreted protein associated polypeptide #18.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 117; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
RESULT 368
ID ABB70857 standard; protein; 929 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39363.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.5%; Score 93.5; DB 4; Length 929;
Best Local Similarity 28.8%; Pred. No. 0.99;
RESULT 369
ID ABB72288 standard; protein; 545 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 500.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 8.3%; Score 91.5; DB 5; Length 545;
Best Local Similarity 20.4%; Pred. No. 0.79;
RESULT 370
ID ABB72300 standard; protein; 688 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 624.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 8.3%; Score 91.5; DB 5; Length 688;
Best Local Similarity 20.4%; Pred. No. 1.1;
RESULT 371
ID AAB50087 standard; protein; 1188 AA.
DE Murine A259.
PN WO200073339-A1.
PD 07-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 91.5; DB 4; Length 1188;
Best Local Similarity 20.5%; Pred. No. 2.3;
RESULT 372
ID AAU10552 standard; protein; 1188 AA.
DE Murine A259 polypeptide.
PN WO200181414-A2.
PD 01-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 91.5; DB 5; Length 1188;
Best Local Similarity 20.5%; Pred. No. 2.3;
RESULT 373
ID AAY36577 standard; protein; 25 AA.
DE Fragment of human secreted protein encoded by gene 42.
PN WO9931117-A1.
PD 24-JUN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 90; DB 2; Length 25;
Best Local Similarity 78.3%; Pred. No. 0.016;
RESULT 374
ID ADA11747 standard; protein; 25 AA.
DE Human novel secreted protein associated polypeptide #17.
PN US2003055236-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.2%; Score 90; DB 6; Length 25;
Best Local Similarity 78.3%; Pred. No. 0.016;
RESULT 375
ID AAW25639 standard; protein; 799 AA.
DE Rat full length cadherin-8.
PN US5646250-A.
PD 08-JUL-1997.
PA (DOHE-) DOHENY EYE INST.
Query Match 8.2%; Score 90; DB 2; Length 799;
Best Local Similarity 21.4%; Pred. No. 2;
RESULT 376
ID AAW13126 standard; protein; 799 AA.
DE Full length rat cadherin-8.
PN US5597725-A.
PD 28-JAN-1997.
PA (DOHE-) DOHENY EYE INST.
Query Match 8.2%; Score 90; DB 2; Length 799;
Best Local Similarity 21.4%; Pred. No. 2;
RESULT 377
ID AAW25635 standard; protein; 793 AA.
DE Human cadherin-8.
PN US5646250-A.
PD 08-JUL-1997.
PA (DOHE-) DOHENY EYE INST.
Query Match 8.1%; Score 89.5; DB 2; Length 793;
Best Local Similarity 20.6%; Pred. No. 2.2;
RESULT 378
ID AAW13132 standard; protein; 793 AA.
DE Full length human cadherin-8.
PN US5597725-A.
PD 28-JAN-1997.
PA (DOHE-) DOHENY EYE INST.
Query Match 8.1%; Score 89.5; DB 2; Length 793;
Best Local Similarity 20.6%; Pred. No. 2.2;
RESULT 379
ID AAM39241 standard; protein; 1035 AA.
DE Human polypeptide SEQ ID NO 2386.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.1%; Score 89.5; DB 4; Length 1035;
Best Local Similarity 20.2%; Pred. No. 3.2;
RESULT 380
ID AAM41027 standard; protein; 1044 AA.
DE Human polypeptide SEQ ID NO 5958.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.1%; Score 89.5; DB 4; Length 1044;
Best Local Similarity 20.2%; Pred. No. 3.3;
RESULT 381
ID AAE20902 standard; protein; 1063 AA.
DE Human INTG-1 protein.
PN WO200212339-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.1%; Score 89.5; DB 5; Length 1063;
Best Local Similarity 20.2%; Pred. No. 3.3;
RESULT 382
ID ABJ19350 standard; protein; 1063 AA.
DE NOVX related protein SEQ ID No 66.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 89.5; DB 6; Length 1063;
Best Local Similarity 20.2%; Pred. No. 3.3;
RESULT 383
ID ADO41700 standard; protein; 1063 AA.

DE Novel human polypeptide NOV24b.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 8.1%; Score 89.5; DB 8; Length 1063;
Best Local Similarity 20.2%; Pred. No. 3.3;
RESULT 384
ID ADG42065 standard; protein; 799 AA.
DE Human CDH8 amino acid sequence.
PN WO2003087408-A2.
PD 23-OCT-2003.
PA (UYED-) UNIV EDINBURGH.
Query Match 8.1%; Score 89; DB 7; Length 799;
Best Local Similarity 21.4%; Pred. No. 2.6;
RESULT 385
ID ADP26902 standard; protein; 799 AA.
DE Human cadherin 8 protein SEQ ID NO:3.
PN EP1428893-A2.
PD 16-JUN-2004.
PA (SPRE/) SPRECHER E.
PA (BERG/) BERGMAN R.
Query Match 8.1%; Score 89; DB 8; Length 799;
Best Local Similarity 21.4%; Pred. No. 2.6;
RESULT 386
ID ABJ19349 standard; protein; 1063 AA.
DE NOVX related protein SEQ ID No 64.
PN WO200299062-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 88.5; DB 6; Length 1063;
Best Local Similarity 20.2%; Pred. No. 4.3;
RESULT 387
ID ADO41698 standard; protein; 1063 AA.
DE Novel human polypeptide NOV24a.
PN US2004018555-A1.
PD 29-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (ZERH/) ZERHUSEN B D.
PA (LILL/) LI L.
PA (ZHON/) ZHONG M.
PA (CASM/) CASMAN S J.
PA (GERL/) GERLACH V.
PA (SHIM/) SHIMKETS R A.
PA (GORM/) GORMAN L.
PA (PENA/) PENA C E A.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (LEIT/) LEITE M W.
PA (RAST/) RASTELLI L.
PA (MACD/) MACDOUGALL J R.
PA (TAUP/) TAUPIER R J.
PA (GUOX/) GUO X S.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (HJAL/) HJALT T.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (MALY/) MALYANKAR U M.
PA (PADI/) PADIGARU M.
PA (JIWW/) JI W.
PA (SMIT/) SMITHSON G.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (ELLE/) ELLERMAN K.
Query Match 8.0%; Score 88.5; DB 8; Length 1063;
Best Local Similarity 20.2%; Pred. No. 4.3;
RESULT 388
ID AAB30929 standard; protein; 1188 AA.
DE Amino acid sequence of a human alpha11 integrin chain.
PN WO200075187-A1.
PD 14-DEC-2000.
PA (ACTI-) ACTIVE BIOTECH AB.
Query Match 8.0%; Score 88.5; DB 4; Length 1188;
Best Local Similarity 22.6%; Pred. No. 5.1;
RESULT 389
ID ABR33337 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1690.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 8.0%; Score 88; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
RESULT 390
ID ABR33285 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1638.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 8.0%; Score 88; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.013;
RESULT 391
ID ABU79109 standard; protein; 365 AA.
DE CD44 protein.
PN US2002177551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.
Query Match 8.0%; Score 88; DB 6; Length 365;
Best Local Similarity 21.6%; Pred. No. 1.1;
RESULT 392
ID ADF43353 standard; protein; 365 AA.
DE CD44 receptor polypeptide seq id 73.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.
Query Match 8.0%; Score 88; DB 7; Length 365;
Best Local Similarity 21.6%; Pred. No. 1.1;
RESULT 393
ID ABB60068 standard; protein; 968 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6996.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.8%; Score 86.5; DB 4; Length 968;
Best Local Similarity 19.1%; Pred. No. 6.3;
RESULT 394
ID ABR33291 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1644.

PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.8%; Score 86; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.021;
RESULT 395
ID ABR33284 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1637.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.8%; Score 86; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.021;
RESULT 396
ID ABR33406 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1759.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.8%; Score 86; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.021;
RESULT 397
ID ABR33375 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1728.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.8%; Score 86; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.021;
RESULT 398
ID ABR33324 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1677.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.8%; Score 86; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.021;
RESULT 399
ID ABR33382 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1735.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.8%; Score 86; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.021;
RESULT 400
ID ABB81033 standard; protein; 364 AA.
DE Rat glycoprotein CD44 polypeptide.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 7.8%; Score 86; DB 5; Length 364;
Best Local Similarity 20.7%; Pred. No. 1.8;
RESULT 401
ID AAR14768 standard; protein; 503 AA.
DE Metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Query Match 7.8%; Score 86; DB 2; Length 503;
Best Local Similarity 20.7%; Pred. No. 2.9;
RESULT 402
ID ADE57911 standard; protein; 503 AA.
DE Rat Protein P26051, SEQ ID NO 3777.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.8%; Score 86; DB 7; Length 503;
Best Local Similarity 20.7%; Pred. No. 2.9;
RESULT 403
ID ABP77872 standard; protein; 468 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 2274.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 7.8%; Score 85.5; DB 6; Length 468;
Best Local Similarity 24.1%; Pred. No. 3;
RESULT 404
ID AAU31438 standard; protein; 543 AA.
DE Novel human secreted protein #1929.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.8%; Score 85.5; DB 4; Length 543;
Best Local Similarity 19.8%; Pred. No. 3.6;
RESULT 405
ID ABB92524 standard; protein; 667 AA.
DE Herbicidally active polypeptide SEQ ID NO 1735.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 7.8%; Score 85.5; DB 5; Length 667;
Best Local Similarity 21.6%; Pred. No. 4.9;
RESULT 406
ID AAB95836 standard; protein; 1148 AA.
DE Human protein sequence SEQ ID NO:18865.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.8%; Score 85.5; DB 4; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 407
ID ABB50283 standard; protein; 1148 AA.
DE HOST-1 ovarian tumour marker protein, SEQ ID NO:56.
PN WO200175177-A2.
PD 11-OCT-2001.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 7.8%; Score 85.5; DB 4; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 408
ID ABG96380 standard; protein; 1148 AA.
DE Human ovarian cancer marker M461.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.8%; Score 85.5; DB 5; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 409
ID ABP30964 standard; protein; 1148 AA.
DE Truncated version protein with sequence homology to 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.8%; Score 85.5; DB 5; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 410
ID ABP30969 standard; protein; 1148 AA.
DE Clone FLJ14303.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.8%; Score 85.5; DB 5; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 411
ID ADA08632 standard; protein; 1148 AA.
DE Human O772P partial protein #2.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.

PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.8%; Score 85.5; DB 7; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 412
ID ADA08611 standard; protein; 1148 AA.
DE Human O772P homology protein #1.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.8%; Score 85.5; DB 7; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 413
ID ADF08954 standard; protein; 1148 AA.
DE Secreted ovarian carcinoma antigen seqid 458.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.8%; Score 85.5; DB 7; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 414
ID ADF08975 standard; protein; 1148 AA.
DE Secreted ovarian carcinoma antigen seqid 479.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.8%; Score 85.5; DB 7; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 415
ID ADG46241 standard; protein; 1148 AA.
DE Human ovarian carcinoma polypeptide #47.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Query Match 7.8%; Score 85.5; DB 7; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 416
ID ADM30754 standard; protein; 1148 AA.
DE Human cancer linked protein referred to as 222520 SeqID 2.
PN WO2003075854-A2.
PD 18-SEP-2003.
PA (AVAL-) AVALON PHARM.
Query Match 7.8%; Score 85.5; DB 7; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 417
ID ADQ29705 standard; protein; 1148 AA.
DE Human colorectal cancer-associated protein #60.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.8%; Score 85.5; DB 8; Length 1148;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 418
ID ABP30965 standard; protein; 1156 AA.
DE Protein with sequence homology to 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.8%; Score 85.5; DB 5; Length 1156;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 419
ID ADA08612 standard; protein; 1156 AA.
DE Human O772P homology protein #2.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.8%; Score 85.5; DB 7; Length 1156;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 420
ID ADF08955 standard; protein; 1156 AA.
DE Secreted ovarian carcinoma antigen seqid 459.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.8%; Score 85.5; DB 7; Length 1156;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 421
ID ADG46242 standard; protein; 1156 AA.
DE Human ovarian carcinoma polypeptide #48.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Query Match 7.8%; Score 85.5; DB 7; Length 1156;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 422
ID ABR58656 standard; protein; 1482 AA.
DE Human cancer related protein SEQ ID NO:313.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.8%; Score 85.5; DB 6; Length 1482;
Best Local Similarity 22.3%; Pred. No. 15;
RESULT 423
ID ABP69627 standard; protein; 1497 AA.
DE Human polypeptide SEQ ID NO 1674.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.8%; Score 85.5; DB 5; Length 1497;
Best Local Similarity 22.3%; Pred. No. 15;
RESULT 424
ID AAE34700 standard; protein; 1889 AA.
DE Protein encoded by B4 DNA clone (CA125).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 7.8%; Score 85.5; DB 6; Length 1889;
Best Local Similarity 21.4%; Pred. No. 21;
RESULT 425
ID ABR33304 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1657.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 426
ID ABR33390 standard; peptide; 15 AA.

DE Human cancer-related protein 156P5C12 HLA peptide #1743.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 427
ID ABR33438 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1791.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 428
ID ABR33367 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1720.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 429
ID ABR33395 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1748.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 430
ID ABR33321 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1674.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 431
ID ABR33400 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1753.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 432
ID ABR33317 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1670.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 433
ID ABR33136 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1354.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 434
ID ABR33087 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1305.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 435
ID ABR33108 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1326.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 436
ID ABR33325 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1678.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.7%; Score 85; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
RESULT 437
ID ADL16195 standard; protein; 1337 AA.
DE Human protein tyrosine phosphatase #14.
PN WO2003068984-A2.
PD 21-AUG-2003.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
Query Match 7.7%; Score 85; DB 7; Length 1337;
Best Local Similarity 20.5%; Pred. No. 15;
RESULT 438
ID AAY75167 standard; protein; 468 AA.
DE Neisseria meningitidis ORF 585 protein sequence SEQ ID NO:1808.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 7.7%; Score 84.5; DB 3; Length 468;
Best Local Similarity 23.7%; Pred. No. 3.8;
RESULT 439
ID AAU14467 standard; protein; 1188 AA.
DE Human novel protein #338.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.7%; Score 84.5; DB 4; Length 1188;
Best Local Similarity 22.5%; Pred. No. 14;
RESULT 440
ID AAU14231 standard; protein; 1188 AA.
DE Human novel protein #102.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.7%; Score 84.5; DB 4; Length 1188;
Best Local Similarity 22.5%; Pred. No. 14;
RESULT 441
ID AAB50085 standard; protein; 1188 AA.
DE Human A259.
PN WO200073339-A1.
PD 07-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.7%; Score 84.5; DB 4; Length 1188;
Best Local Similarity 22.5%; Pred. No. 14;
RESULT 442
ID AAU10551 standard; protein; 1188 AA.
DE Human A259 polypeptide.
PN WO200181414-A2.
PD 01-NOV-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.7%; Score 84.5; DB 5; Length 1188;
Best Local Similarity 22.5%; Pred. No. 14;
RESULT 443
ID ADE09956 standard; protein; 1188 AA.
DE Novel protein-related contig polypeptide sequence #544.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.7%; Score 84.5; DB 7; Length 1188;
Best Local Similarity 22.5%; Pred. No. 14;
RESULT 444
ID ABR33383 standard; peptide; 15 AA.

DE Human cancer-related protein 156P5C12 HLA peptide #1736.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.6%; Score 84; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
RESULT 445
ID ABR33116 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1334.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.6%; Score 84; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
RESULT 446
ID ABR33302 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1655.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.6%; Score 84; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
RESULT 447
ID ABR33452 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1805.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.6%; Score 84; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
RESULT 448
ID ABR33126 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1344.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.6%; Score 84; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
RESULT 449
ID ABR33314 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1667.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.6%; Score 84; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
RESULT 450
ID AAR85203 standard; protein; 1337 AA.
DE huDEP-1.
PN WO9530008-A1.
PD 09-NOV-1995.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 7.6%; Score 83.5; DB 2; Length 1337;
Best Local Similarity 26.4%; Pred. No. 21;
RESULT 451
ID ADL16193 standard; protein; 1337 AA.
DE Human protein tyrosine phosphatase #13.
PN WO2003068984-A2.
PD 21-AUG-2003.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
Query Match 7.6%; Score 83.5; DB 7; Length 1337;
Best Local Similarity 26.4%; Pred. No. 21;
RESULT 452
ID ADP74603 standard; protein; 1337 AA.
DE Amino acid sequence of human DEP-1.
PN WO2004048549-A2.
PD 10-JUN-2004.
PA (COLD-) COLD SPRING HARBOR LAB.
Query Match 7.6%; Score 83.5; DB 8; Length 1337;
Best Local Similarity 26.4%; Pred. No. 21;
RESULT 453
ID ABR33125 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1343.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.5%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.046;
RESULT 454
ID ABR33398 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1751.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.5%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.046;
RESULT 455
ID ABR33351 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1704.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.5%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.046;
RESULT 456
ID ABR33297 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1650.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.5%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.046;
RESULT 457
ID ABR33427 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1780.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.5%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.046;
RESULT 458
ID ABR33115 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1333.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.5%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.046;
RESULT 459
ID ABR33336 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1689.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.5%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.046;
RESULT 460
ID ABR33363 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1716.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.5%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.046;
RESULT 461
ID ABR33113 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1331.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.5%; Score 83; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.046;
RESULT 462
ID AAY75165 standard; protein; 231 AA.
DE Neisseria gonorrheae ORF 585 protein sequence SEQ ID NO:1804.

PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 7.5%; Score 82.5; DB 3; Length 231;
Best Local Similarity 24.1%; Pred. No. 2.4;
RESULT 463
ID ADH88063 standard; protein; 529 AA.
DE Enterococcus faecalis polypeptide #2543.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 7.5%; Score 82.5; DB 7; Length 529;
Best Local Similarity 24.7%; Pred. No. 7.6;
RESULT 464
ID ADS94303 standard; protein; 809 AA.
DE CA 125/O772P 3-repeat TM amino acid sequence SEQ ID NO:2.
PN WO2004035537-A2.
PD 29-APR-2004.
PA (EURO-) EUROCELTIQUE SA.
Query Match 7.5%; Score 82.5; DB 8; Length 809;
Best Local Similarity 20.3%; Pred. No. 14;
RESULT 465
ID ABR33323 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1676.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 466
ID ABR33397 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1750.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 467
ID ABR33084 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1302.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 468
ID ABR33296 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1649.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 469
ID ABR33290 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1643.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 470
ID ABR33313 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1666.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 471
ID ABR33391 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1744.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 472
ID ABR33109 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1327.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 473
ID ABR33373 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1726.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 474
ID ABR33436 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1789.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 475
ID ABR33097 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1315.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 476
ID ABR33420 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1773.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 82; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.059;
RESULT 477
ID ABR58365 standard; protein; 1120 AA.
DE Human NOV2b.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 82; DB 6; Length 1120;
Best Local Similarity 21.4%; Pred. No. 25;
RESULT 478
ID AAB25582 standard; protein; 1189 AA.
DE ITGA11 protein encoded by human secreted protein gene #7.
PN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.4%; Score 82; DB 3; Length 1189;
Best Local Similarity 21.4%; Pred. No. 27;
RESULT 479
ID ABR58364 standard; protein; 1189 AA.
DE Human NOV2a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 82; DB 6; Length 1189;
Best Local Similarity 21.4%; Pred. No. 27;
RESULT 480
ID ADA27054 standard; protein; 1189 AA.
DE Human novel secreted protein from cDNA HOHBY69 #1.

PN US2003055231-A1.
PD 20-MAR-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
PA (LIUD/) LIU D.
PA (CROC/) CROCKER P R.
Query Match 7.4%; Score 82; DB 6; Length 1189;
Best Local Similarity 21.4%; Pred. No. 27;
RESULT 481
ID ADE63570 standard; protein; 1189 AA.
DE Human Protein Q9UKX5, SEQ ID NO 9514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.4%; Score 82; DB 7; Length 1189;
Best Local Similarity 21.4%; Pred. No. 27;
RESULT 482
ID ADE86584 standard; protein; 1189 AA.
DE Novel human secreted protein #7.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Query Match 7.4%; Score 82; DB 8; Length 1189;
Best Local Similarity 21.4%; Pred. No. 27;
RESULT 483
ID ADQ19968 standard; protein; 1189 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2788.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.4%; Score 82; DB 8; Length 1189;
Best Local Similarity 21.4%; Pred. No. 27;
RESULT 484
ID ADL16200 standard; protein; 1216 AA.
DE Rat protein tyrosine phosphatase #4.
PN WO2003068984-A2.
PD 21-AUG-2003.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
Query Match 7.4%; Score 82; DB 7; Length 1216;
Best Local Similarity 26.7%; Pred. No. 28;
RESULT 485
ID ABP68575 standard; protein; 302 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:268.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 7.4%; Score 81.5; DB 5; Length 302;
Best Local Similarity 23.9%; Pred. No. 4.5;
RESULT 486
ID ADM18903 standard; protein; 302 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:268.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 7.4%; Score 81.5; DB 8; Length 302;
Best Local Similarity 23.9%; Pred. No. 4.5;
RESULT 487
ID ABM69195 standard; protein; 364 AA.
DE Photorhabdus luminescens protein sequence #2292.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 7.4%; Score 81.5; DB 6; Length 364;
Best Local Similarity 25.0%; Pred. No. 5.8;
RESULT 488
ID AAU76335 standard; peptide; 1048 AA.
DE Human anti-dual integrin protein #1.
PN WO200212501-A2.
PD 14-FEB-2002.
PA (CENZ) CENTOCOR INC.
Query Match 7.4%; Score 81.5; DB 5; Length 1048;
Best Local Similarity 23.7%; Pred. No. 25;
RESULT 489
ID ABU03549 standard; protein; 1048 AA.
DE Angiogenesis-associated human protein sequence #94.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.4%; Score 81.5; DB 6; Length 1048;
Best Local Similarity 23.7%; Pred. No. 25;
RESULT 490
ID AAO27098 standard; protein; 1048 AA.
DE Human integrin alpha-V precursor (CD51).
PN WO2003010190-A2.
PD 06-FEB-2003.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA (BIOA-) BIOACTA LTD.
Query Match 7.4%; Score 81.5; DB 6; Length 1048;
Best Local Similarity 23.7%; Pred. No. 25;
RESULT 491
ID ABB82767 standard; protein; 1048 AA.
DE Human alphaVbeta3 integrin alphaV subunit sequence.
PN WO200287505-A2.
PD 07-NOV-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.4%; Score 81.5; DB 6; Length 1048;
Best Local Similarity 23.7%; Pred. No. 25;
RESULT 492
ID ADD48891 standard; protein; 1048 AA.
DE Human Protein NP_002201, SEQ ID NO 14602.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.4%; Score 81.5; DB 7; Length 1048;
Best Local Similarity 23.7%; Pred. No. 25;
RESULT 493
ID ABG18895 standard; protein; 1061 AA.
DE Novel human diagnostic protein #18886.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.4%; Score 81.5; DB 4; Length 1061;
Best Local Similarity 23.7%; Pred. No. 26;
RESULT 494
ID ABR33098 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1316.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 495
ID ABR33369 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1722.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 496
ID ABR33370 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1723.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 497
ID ABR33419 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1772.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 498
ID ABR33341 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1694.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 499
ID ABR33309 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1662.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 500
ID ABR33384 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1737.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 501
ID ABR33107 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1325.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 502
ID ABR33371 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1724.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 503
ID ABR33404 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1757.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 504
ID ABR33408 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1761.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 505
ID ABR33428 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1781.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 506
ID ABR33387 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1740.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 507
ID ABR33443 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1796.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 508
ID ABR33447 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1800.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 509
ID ABR33300 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1653.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 510
ID ABR33083 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1301.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.4%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.076;
RESULT 511
ID ABU54859 standard; protein; 284 AA.
DE Human CA125 carboxy terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 80.5; DB 6; Length 284;
Best Local Similarity 20.8%; Pred. No. 5.3;
RESULT 512
ID AAE12623 standard; protein; 438 AA.
DE Human gene 1 encoded secreted protein HIPAZ30.
PN WO200170804-A1.
PD 27-SEP-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 80.5; DB 4; Length 438;
Best Local Similarity 20.8%; Pred. No. 9.7;
RESULT 513
ID ABP30973 standard; protein; 438 AA.
DE Partial protein sequence of clone 0772P partial cDNA sequence 4.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.3%; Score 80.5; DB 5; Length 438;
Best Local Similarity 20.8%; Pred. No. 9.7;
RESULT 514

ID ADA08636 standard; protein; 438 AA.
DE Human O772P partial protein #6.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.3%; Score 80.5; DB 7; Length 438;
Best Local Similarity 20.8%; Pred. No. 9.7;
RESULT 515
ID ADF08979 standard; protein; 438 AA.
DE Secreted ovarian carcinoma antigen seqid 483.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.3%; Score 80.5; DB 7; Length 438;
Best Local Similarity 20.8%; Pred. No. 9.7;
RESULT 516
ID ABU54709 standard; protein; 439 AA.
DE Human CA125 protein carboxy terminus.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 80.5; DB 6; Length 439;
Best Local Similarity 20.8%; Pred. No. 9.7;
RESULT 517
ID AAE12634 standard; protein; 526 AA.
DE Human gene 1 encoded secreted protein fragment, SEQ ID NO: 30.
PN WO200170804-A1.
PD 27-SEP-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 80.5; DB 4; Length 526;
Best Local Similarity 20.8%; Pred. No. 13;
RESULT 518
ID ABB93901 standard; protein; 675 AA.
DE Herbicidally active polypeptide SEQ ID NO 3112.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 7.3%; Score 80.5; DB 5; Length 675;
Best Local Similarity 26.6%; Pred. No. 18;
RESULT 519
ID ABU54692 standard; protein; 1148 AA.
DE Human CA125 protein from cDNA AK024365.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 80.5; DB 6; Length 1148;
Best Local Similarity 20.8%; Pred. No. 37;
RESULT 520
ID ABU00145 standard; protein; 1148 AA.
DE Human novel polypeptide #238.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 80.5; DB 6; Length 1148;
Best Local Similarity 20.8%; Pred. No. 37;
RESULT 521
ID ADH41326 standard; protein; 1148 AA.
DE Human ovarian specific gene (OSG) protein.
PN US2003096238-A1.
PD 22-MAY-2003.
PA (SALC/) SALCEDA S.
PA (CAFF/) CAFFERKEY R.
Query Match 7.3%; Score 80.5; DB 8; Length 1148;
Best Local Similarity 20.8%; Pred. No. 37;
RESULT 522
ID ADR10190 standard; protein; 1307 AA.
DE Human protein useful for treating neurological disease Seq 3696.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.3%; Score 80.5; DB 8; Length 1307;
Best Local Similarity 20.8%; Pred. No. 45;
RESULT 523
ID ABU54693 standard; protein; 2248 AA.
DE Human CA125 protein with 13 repeats and the carboxy terminus.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 80.5; DB 6; Length 2248;
Best Local Similarity 20.8%; Pred. No. 96;
RESULT 524
ID ABU54721 standard; protein; 11721 AA.
DE Human CA125 full length protein sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 80.5; DB 6; Length 11721;
Best Local Similarity 20.8%; Pred. No. 9.6e+02;
RESULT 525
ID ADR72871 standard; protein; 22152 AA.
DE Human ovarian cancer-related tumour marker CA125 protein.
PN WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 7.3%; Score 80.5; DB 8; Length 22152;
Best Local Similarity 20.8%; Pred. No. 2.3e+03;
RESULT 526
ID ADP84155 standard; protein; 22157 AA.
DE Human CA125 protein sequence SeqID 5.
PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.3%; Score 80.5; DB 8; Length 22157;
Best Local Similarity 20.8%; Pred. No. 2.3e+03;
RESULT 527
ID ABR33122 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1340.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.3%; Score 80; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.098;
RESULT 528
ID ABR33372 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1725.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.3%; Score 80; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.098;
RESULT 529
ID ABR33434 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1787.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.3%; Score 80; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.098;
RESULT 530
ID ABR33435 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1788.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.3%; Score 80; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.098;

RESULT 531
ID ABR33310 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1663.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.3%; Score 80; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.098;
RESULT 532
ID ABR33414 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1767.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.3%; Score 80; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.098;
RESULT 533
ID ABR33132 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1350.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.3%; Score 80; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.098;
RESULT 534
ID ABR33354 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1707.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.3%; Score 80; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.098;
RESULT 535
ID ABR33358 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1711.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.3%; Score 80; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.098;
RESULT 536
ID ABG18894 standard; protein; 156 AA.
DE Novel human diagnostic protein #18885.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.2%; Score 79.5; DB 4; Length 156;
Best Local Similarity 22.1%; Pred. No. 3;
RESULT 537
ID ADN17692 standard; protein; 355 AA.
DE Bacterial polypeptide #345.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.2%; Score 79.5; DB 8; Length 355;
Best Local Similarity 23.2%; Pred. No. 9.3;
RESULT 538
ID ABG96381 standard; protein; 1890 AA.
DE Human ovarian cancer marker M612.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.2%; Score 79.5; DB 5; Length 1890;
Best Local Similarity 20.8%; Pred. No. 97;
RESULT 539
ID ADM12352 standard; protein; 1890 AA.
DE Human CA125 ovarian cancer antigen mucin 16 protein.
PN US2003235594-A1.
PD 25-DEC-2003.
PA (ANTI-) ANTIGEN EXPRESS INC.
Query Match 7.2%; Score 79.5; DB 8; Length 1890;
Best Local Similarity 20.8%; Pred. No. 97;
RESULT 540
ID ADO38574 standard; protein; 1890 AA.
DE Ovarian cancer antigen CA125.
PN US2004058881-A1.
PD 25-MAR-2004.
PA (ANTI-) ANTIGEN EXPRESS INC.
Query Match 7.2%; Score 79.5; DB 8; Length 1890;
Best Local Similarity 20.8%; Pred. No. 97;
RESULT 541
ID ADJ66747 standard; protein; 2234 AA.
DE Human Muc16 GST fusion protein amino acid sequence SeqID20.
PN WO2004005470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
Query Match 7.2%; Score 79.5; DB 8; Length 2234;
Best Local Similarity 20.8%; Pred. No. 1.2e+02;
RESULT 542
ID ABR33288 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1641.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.2%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
RESULT 543
ID ABR33298 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1651.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.2%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
RESULT 544
ID ABR33412 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1765.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.2%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
RESULT 545
ID ABR33103 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1321.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.2%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
RESULT 546
ID ABR33319 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1672.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.2%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
RESULT 547
ID ABR33305 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1658.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.2%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
RESULT 548
ID ABR33355 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1708.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.

Query Match 7.2%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
RESULT 549
ID ABR33381 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1734.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.2%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
RESULT 550
ID ABR33139 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1357.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.2%; Score 79; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.13;
RESULT 551
ID ABG12949 standard; protein; 1189 AA.
DE Novel human diagnostic protein #12940.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.2%; Score 79; DB 4; Length 1189;
Best Local Similarity 21.8%; Pred. No. 58;
RESULT 552
ID ABB71928 standard; protein; 2037 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 42576.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.2%; Score 79; DB 4; Length 2037;
Best Local Similarity 24.5%; Pred. No. 1.2e+02;
RESULT 553
ID ABP30978 standard; protein; 233 AA.
DE Extracellular and transmembranal regions of 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 5; Length 233;
Best Local Similarity 21.5%; Pred. No. 6.7;
RESULT 554
ID ADA08641 standard; protein; 233 AA.
DE Human O772P partial protein #11.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.1%; Score 78.5; DB 7; Length 233;
Best Local Similarity 21.5%; Pred. No. 6.7;
RESULT 555
ID ADF08984 standard; peptide; 233 AA.
DE Secreted ovarian carcinoma antigen seqid 488.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 7; Length 233;
Best Local Similarity 21.5%; Pred. No. 6.7;
RESULT 556
ID ABP31025 standard; protein; 318 AA.
DE Amino acid sequence of the 3' constant region of 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 5; Length 318;
Best Local Similarity 20.8%; Pred. No. 10;
RESULT 557
ID ADA08747 standard; protein; 318 AA.
DE Human O772P constant region consensus sequence #1.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.1%; Score 78.5; DB 7; Length 318;
Best Local Similarity 20.8%; Pred. No. 10;
RESULT 558
ID ADF09090 standard; protein; 318 AA.
DE Secreted ovarian carcinoma antigen seqid 594.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 7; Length 318;
Best Local Similarity 20.8%; Pred. No. 10;
RESULT 559
ID AAB42399 standard; protein; 336 AA.
DE Human ORFX ORF2163 polypeptide sequence SEQ ID NO:4326.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 7.1%; Score 78.5; DB 3; Length 336;
Best Local Similarity 22.1%; Pred. No. 11;
RESULT 560
ID AAB12555 standard; protein; 438 AA.
DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:390.
PN WO200036107-A2.
PD 22-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 3; Length 438;
Best Local Similarity 21.5%; Pred. No. 16;
RESULT 561
ID ABP30899 standard; protein; 438 AA.
DE 0772P clone 21008.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 5; Length 438;
Best Local Similarity 21.5%; Pred. No. 16;
RESULT 562
ID ADA08543 standard; protein; 438 AA.
DE Human ovarian carcinoma antigen O772P #3.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.1%; Score 78.5; DB 7; Length 438;
Best Local Similarity 21.5%; Pred. No. 16;
RESULT 563
ID ADF08886 standard; protein; 438 AA.

DE Secreted ovarian carcinoma antigen seqid 390.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 7; Length 438;
Best Local Similarity 21.5%; Pred. No. 16;
RESULT 564
ID ADG46173 standard; protein; 438 AA.
DE Human ovarian carcinoma polypeptide #4.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Query Match 7.1%; Score 78.5; DB 7; Length 438;
Best Local Similarity 21.5%; Pred. No. 16;
RESULT 565
ID ABB72289 standard; protein; 696 AA.
DE Rat protein isolated from skin cells SEQ ID NO: 501.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 7.1%; Score 78.5; DB 5; Length 696;
Best Local Similarity 19.7%; Pred. No. 31;
RESULT 566
ID AAB12554 standard; protein; 833 AA.
DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:389.
PN WO200036107-A2.
PD 22-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 3; Length 833;
Best Local Similarity 21.5%; Pred. No. 40;
RESULT 567
ID ABP30898 standard; protein; 833 AA.
DE 0772P clone 21003.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 5; Length 833;
Best Local Similarity 21.5%; Pred. No. 40;
RESULT 568
ID ADA08542 standard; protein; 833 AA.
DE Human ovarian carcinoma antigen O772P #2.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.1%; Score 78.5; DB 7; Length 833;
Best Local Similarity 21.5%; Pred. No. 40;
RESULT 569
ID ADF08885 standard; protein; 833 AA.
DE Secreted ovarian carcinoma antigen seqid 389.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 7; Length 833;
Best Local Similarity 21.5%; Pred. No. 40;
RESULT 570
ID ADG46172 standard; protein; 833 AA.
DE Human ovarian carcinoma polypeptide #3.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Query Match 7.1%; Score 78.5; DB 7; Length 833;
Best Local Similarity 21.5%; Pred. No. 40;
RESULT 571
ID AAB12552 standard; protein; 914 AA.
DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:312.
PN WO200036107-A2.
PD 22-JUN-2000.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 3; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 572
ID AAB99203 standard; protein; 914 AA.
DE Human ovarian tumour-derived antigen O772P.
PN WO200140269-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 4; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 573
ID ABP30968 standard; protein; 914 AA.
DE Hypothetical protein sequence for clone 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 5; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 574
ID ABP30896 standard; protein; 914 AA.
DE 0772P protein.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 5; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 575
ID ADA08631 standard; protein; 914 AA.
DE Human O772P partial protein #1.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.1%; Score 78.5; DB 7; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 576
ID ADA08465 standard; protein; 914 AA.
DE Human ovarian carcinoma antigen O772P.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.1%; Score 78.5; DB 7; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 577
ID ADF08974 standard; protein; 914 AA.
DE Secreted ovarian carcinoma antigen seqid 478.
PN US2003124140-A1.

PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 7; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 578
ID ADF08808 standard; protein; 914 AA.
DE Secreted ovarian carcinoma antigen seqid 312.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 7; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 579
ID ADG46095 standard; protein; 914 AA.
DE Human ovarian carcinoma polypeptide #1.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Query Match 7.1%; Score 78.5; DB 7; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 580
ID ADN40451 standard; protein; 914 AA.
DE Human breast cancer associated polypeptide sequence #4.
PN US2004101899-A1.
PD 27-MAY-2004.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 8; Length 914;
Best Local Similarity 21.5%; Pred. No. 45;
RESULT 581
ID ABB58394 standard; protein; 970 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1974.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.1%; Score 78.5; DB 4; Length 970;
Best Local Similarity 24.5%; Pred. No. 49;
RESULT 582
ID ABP31026 standard; protein; 3451 AA.
DE Amino acid sequence containing consensus and 3' region of 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 5; Length 3451;
Best Local Similarity 20.8%; Pred. No. 2.9e+02;
RESULT 583
ID ADA08748 standard; protein; 3451 AA.
DE Human O772P consensus sequence #1.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Query Match 7.1%; Score 78.5; DB 7; Length 3451;
Best Local Similarity 20.8%; Pred. No. 2.9e+02;
RESULT 584
ID ADF09091 standard; protein; 3451 AA.
DE Secreted ovarian carcinoma antigen seqid 595.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.1%; Score 78.5; DB 7; Length 3451;
Best Local Similarity 20.8%; Pred. No. 2.9e+02;
RESULT 585
ID ABR33306 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1659.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 586
ID ABR33421 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1774.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 587
ID ABR33131 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1349.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 588
ID ABR33312 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1665.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 589
ID ABR33119 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1337.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 590
ID ABR33368 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1721.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 591
ID ABR33385 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1738.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 592
ID ABR33453 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1806.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 593
ID ABR33329 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1682.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 594
ID ABR33299 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1652.

PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 595
ID ABR33342 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1695.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 596
ID ABR33352 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1705.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 597
ID ABR33364 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1717.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 598
ID ABR33378 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1731.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 599
ID ABR33410 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1763.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 600
ID ABR33448 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1801.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 601
ID ABR33090 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1308.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 602
ID ABR33123 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1341.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 603
ID ABR33140 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1358.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 604
ID ABR33145 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1363.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 605
ID ABR33425 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1778.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 606
ID ABR33117 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1335.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 607
ID ABR33332 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1685.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 608
ID ABR33362 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1715.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 609
ID ABR33089 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1307.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 610
ID ABR33418 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1771.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 611
ID ABR33440 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1793.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.1%; Score 78; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.16;
RESULT 612
ID ABP68513 standard; protein; 300 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:196.
PN WO200200717-A2.
PD 03-JAN-2002.

PA (MAXY-) MAXYGEN INC.
Query Match 7.1%; Score 78; DB 5; Length 300;
Best Local Similarity 21.4%; Pred. No. 11;
RESULT 613
ID ADM18831 standard; protein; 300 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:196.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 7.1%; Score 78; DB 8; Length 300;
Best Local Similarity 21.4%; Pred. No. 11;
RESULT 614
ID ABB08348 standard; protein; 343 AA.
DE RTA-like G protein-coupled receptor, SEQ ID NO:3.
PN WO200200699-A1.
PD 03-JAN-2002.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 78; DB 5; Length 343;
Best Local Similarity 20.9%; Pred. No. 13;
RESULT 615
ID ABG73784 standard; protein; 343 AA.
DE Rat RTA orphan receptor protein.
PN US2002150980-A1.
PD 17-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.1%; Score 78; DB 6; Length 343;
Best Local Similarity 20.9%; Pred. No. 13;
RESULT 616
ID ADB12843 standard; protein; 343 AA.
DE Rat orphan G protein-coupled receptor RTA.
PN US2002192760-A1.
PD 19-DEC-2002.
PA (LIYY/) LI Y.
PA (ROSE/) ROSEN C A.
PA (GOCA/) GOCAYNE J D.
Query Match 7.1%; Score 78; DB 6; Length 343;
Best Local Similarity 20.9%; Pred. No. 13;
RESULT 617
ID ABR39948 standard; protein; 354 AA.
DE Human prostate selective polypeptide Pr498.
PN WO2003014298-A2.
PD 20-FEB-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 7.1%; Score 78; DB 6; Length 354;
Best Local Similarity 21.0%; Pred. No. 14;
RESULT 618
ID AAB95230 standard; protein; 555 AA.
DE Human protein sequence SEQ ID NO:17363.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.1%; Score 78; DB 4; Length 555;
Best Local Similarity 21.0%; Pred. No. 26;
RESULT 619
ID AAE22147 standard; protein; 555 AA.
DE Human TRNFR-9 protein.
PN WO200226950-A2.
PD 04-APR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.1%; Score 78; DB 5; Length 555;
Best Local Similarity 21.0%; Pred. No. 26;
RESULT 620
ID ADG93389 standard; protein; 887 AA.
DE Maize lipoxygenase (LOX) polypeptide #10.
PN US2003166855-A1.
PD 04-SEP-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.1%; Score 78; DB 7; Length 887;
Best Local Similarity 24.1%; Pred. No. 49;
RESULT 621
ID ADG93387 standard; protein; 887 AA.
DE Maize lipoxygenase (LOX) polypeptide #9.
PN US2003166855-A1.
PD 04-SEP-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match 7.1%; Score 78; DB 7; Length 887;
Best Local Similarity 24.1%; Pred. No. 49;
RESULT 622
ID AAM78602 standard; protein; 189 AA.
DE Human protein SEQ ID NO 1264.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 77.5; DB 4; Length 189;
Best Local Similarity 19.5%; Pred. No. 6.5;
RESULT 623
ID ADD69604 standard; protein; 232 AA.
DE Human REMAP protein - SEQ ID 33.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.0%; Score 77.5; DB 7; Length 232;
Best Local Similarity 23.3%; Pred. No. 8.6;
RESULT 624
ID AAY75166 standard; protein; 468 AA.
DE Neisseria meningitidis ORF 585 protein sequence SEQ ID NO:1806.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match 7.0%; Score 77.5; DB 3; Length 468;
Best Local Similarity 23.2%; Pred. No. 23;
RESULT 625
ID ABR33096 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1314.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 626
ID ABR33143 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1361.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 627
ID ABR33380 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1733.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 628
ID ABR33405 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1758.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 629
ID ABR33286 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1639.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 630
ID ABR33307 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1660.
PN WO200283921-A2.

PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 631
ID ABR33350 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1703.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 632
ID ABR33359 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1712.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 633
ID ABR33411 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1764.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 634
ID ABR33353 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1706.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 635
ID ABR33379 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1732.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 636
ID ABR33111 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1329.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 637
ID ABR33295 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1648.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 638
ID ABR33403 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1756.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 639
ID ABR33315 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1668.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 640
ID ABR33330 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1683.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 641
ID ABR33442 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1795.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 642
ID ABR33106 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1324.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 7.0%; Score 77; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.21;
RESULT 643
ID AAP80246 standard; protein; 282 AA.
DE Sequence of mouse macrophage Fc-gamma-beta-2 receptor protein for
DE immunoglobulin G (IgG).
PN WO8803172-A.
PD 05-MAY-1988.
PA (SLOK) MEM SLOAN-KETTERING.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 7.0%; Score 77; DB 1; Length 282;
Best Local Similarity 19.6%; Pred. No. 13;
RESULT 644
ID ABP68455 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:59.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 76.5; DB 5; Length 303;
Best Local Similarity 22.6%; Pred. No. 16;
RESULT 645
ID ADM18694 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:59.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 76.5; DB 8; Length 303;
Best Local Similarity 22.6%; Pred. No. 16;
RESULT 646
ID ABP73849 standard; protein; 314 AA.
DE Candida albicans essential protein SEQ ID NO 7686.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.9%; Score 76.5; DB 5; Length 314;
Best Local Similarity 20.0%; Pred. No. 17;
RESULT 647
ID ADN46487 standard; protein; 436 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID365.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.9%; Score 76.5; DB 8; Length 436;
Best Local Similarity 22.6%; Pred. No. 27;
RESULT 648
ID AAE23281 standard; protein; 542 AA.
DE Human deleted nectin-3alpha protein.
PN WO200228902-A2.

PD 11-APR-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 6.9%; Score 76.5; DB 5; Length 542;
Best Local Similarity 25.4%; Pred. No. 36;
RESULT 649
ID AAE23283 standard; protein; 549 AA.
DE Human nectin-3alpha protein.
PN WO200228902-A2.
PD 11-APR-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 6.9%; Score 76.5; DB 5; Length 549;
Best Local Similarity 25.4%; Pred. No. 37;
RESULT 650
ID AAE23282 standard; protein; 549 AA.
DE Mouse nectin-3-human nectin 3alpha fusion protein.
PN WO200228902-A2.
PD 11-APR-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 6.9%; Score 76.5; DB 5; Length 549;
Best Local Similarity 25.4%; Pred. No. 37;
RESULT 651
ID ABJ20222 standard; protein; 549 AA.
DE Human IG gene related protein SEQ ID No 45.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 6.9%; Score 76.5; DB 6; Length 549;
Best Local Similarity 25.4%; Pred. No. 37;
RESULT 652
ID ADR66369 standard; protein; 549 AA.
DE Human prostatic carcinoma derived protein SEQ ID 223 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 6.9%; Score 76.5; DB 8; Length 549;
Best Local Similarity 25.4%; Pred. No. 37;
RESULT 653
ID ADR66711 standard; protein; 549 AA.
DE Human prostatic carcinoma derived protein SEQ ID 223 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 6.9%; Score 76.5; DB 8; Length 549;
Best Local Similarity 25.4%; Pred. No. 37;
RESULT 654
ID ABG18352 standard; protein; 653 AA.
DE Novel human diagnostic protein #18343.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 76.5; DB 4; Length 653;
Best Local Similarity 22.4%; Pred. No. 47;
RESULT 655
ID ADI16948 standard; protein; 794 AA.
DE African clawed frog NOVX protein homologue SeqID 484.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 76.5; DB 5; Length 794;
Best Local Similarity 19.2%; Pred. No. 62;
RESULT 656
ID ABR33335 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1688.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 657
ID ABR33377 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1730.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 658
ID ABR33451 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1804.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 659
ID ABR33318 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1671.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 660
ID ABR33282 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1635.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 661
ID ABR33437 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1790.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 662
ID ABR33101 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1319.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 663
ID ABR33086 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1304.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 664
ID ABR33129 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1347.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 665
ID ABR33392 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1745.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.

Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 666
ID ABR33095 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1313.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 667
ID ABR33415 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1768.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 668
ID ABR33114 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1332.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 669
ID ABR33137 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1355.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 670
ID ABR33326 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1679.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 671
ID ABR33102 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1320.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 672
ID ABR33316 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1669.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 673
ID ABR33439 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1792.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.9%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
RESULT 674
ID AAE37802 standard; protein; 230 AA.
DE Human mucin 1 transmembrane variant, MUC1/X protein.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 6.9%; Score 76; DB 6; Length 230;
Best Local Similarity 21.7%; Pred. No. 12;
RESULT 675
ID ADJ68550 standard; protein; 230 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID356.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.9%; Score 76; DB 7; Length 230;
Best Local Similarity 21.7%; Pred. No. 12;
RESULT 676
ID ADI57756 standard; protein; 230 AA.
DE Human breast specific protein (BSP) #33.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 76; DB 8; Length 230;
Best Local Similarity 21.7%; Pred. No. 12;
RESULT 677
ID ADI57775 standard; protein; 232 AA.
DE Human breast specific protein (BSP) #52.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 76; DB 8; Length 232;
Best Local Similarity 23.1%; Pred. No. 13;
RESULT 678
ID ABB89532 standard; protein; 127 AA.
DE Human polypeptide SEQ ID NO 1908.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 75.5; DB 5; Length 127;
Best Local Similarity 23.0%; Pred. No. 6.2;
RESULT 679
ID AAM15391 standard; protein; 133 AA.
DE Peptide #1825 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 75.5; DB 4; Length 133;
Best Local Similarity 19.2%; Pred. No. 6.6;
RESULT 680
ID ABB34397 standard; peptide; 133 AA.
DE Peptide #1903 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 75.5; DB 4; Length 133;
Best Local Similarity 19.2%; Pred. No. 6.6;
RESULT 681
ID AAM27879 standard; protein; 133 AA.
DE Peptide #1916 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 75.5; DB 4; Length 133;
Best Local Similarity 19.2%; Pred. No. 6.6;
RESULT 682
ID ABB29234 standard; peptide; 133 AA.
DE Peptide #1885 encoded by breast cell single exon nucleic acid probe.
PN WO200157271-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 75.5; DB 4; Length 133;
Best Local Similarity 19.2%; Pred. No. 6.6;
RESULT 683
ID ABB19808 standard; protein; 133 AA.
DE Protein #1807 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 6.9%; Score 75.5; DB 4; Length 133;

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  Best Local Similarity   19.2%;  Pred. No. 6.6;
RESULT 684
ID   AAM67582 standard; protein; 133 AA.
DE   Human bone marrow expressed probe encoded protein SEQ ID NO: 27888.
PN   WO200157276-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match             6.9%;  Score 75.5;  DB 4;  Length 133;
  Best Local Similarity   19.2%;  Pred. No. 6.6;
RESULT 685
ID   AAM55187 standard; protein; 133 AA.
DE   Human brain expressed single exon probe encoded protein SEQ ID NO: 27292.
PN   WO200157275-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match             6.9%;  Score 75.5;  DB 4;  Length 133;
  Best Local Similarity   19.2%;  Pred. No. 6.6;
RESULT 686
ID   ABG49228 standard; peptide; 133 AA.
DE   Human liver peptide, SEQ ID No 27876.
PN   WO200157273-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match             6.9%;  Score 75.5;  DB 4;  Length 133;
  Best Local Similarity   19.2%;  Pred. No. 6.6;
RESULT 687
ID   AAM03153 standard; protein; 133 AA.
DE   Peptide #1835 encoded by probe for measuring breast gene expression.
PN   WO200157270-A2.
PD   09-AUG-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match             6.9%;  Score 75.5;  DB 4;  Length 133;
  Best Local Similarity   19.2%;  Pred. No. 6.6;
RESULT 688
ID   ABG37173 standard; peptide; 133 AA.
DE   Human peptide encoded by genome-derived single exon probe SEQ ID 26838.
PN   WO200186003-A2.
PD   15-NOV-2001.
PA   (MOLE-) MOLECULAR DYNAMICS INC.
  Query Match             6.9%;  Score 75.5;  DB 5;  Length 133;
  Best Local Similarity   19.2%;  Pred. No. 6.6;
RESULT 689
ID   ADI57774 standard; protein; 180 AA.
DE   Human breast specific protein (BSP) #51.
PN   WO2003106648-A2.
PD   24-DEC-2003.
PA   (DIAD-) DIADEXUS INC.
  Query Match             6.9%;  Score 75.5;  DB 8;  Length 180;
  Best Local Similarity   24.2%;  Pred. No. 10;
RESULT 690
ID   AAR89423 standard; protein; 239 AA.
DE   Mucin-derived protein MUC1/V/alt.
PN   WO9603502-A2.
PD   08-FEB-1996.
PA   (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
  Query Match             6.9%;  Score 75.5;  DB 2;  Length 239;
  Best Local Similarity   24.2%;  Pred. No. 15;
RESULT 691
ID   AAR89422 standard; protein; 240 AA.
DE   Mucin-derived protein MUC1/V.
PN   WO9603502-A2.
PD   08-FEB-1996.
PA   (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
  Query Match             6.9%;  Score 75.5;  DB 2;  Length 240;
  Best Local Similarity   24.2%;  Pred. No. 15;
RESULT 692
ID   ADE48140 standard; protein; 240 AA.
DE   MUC1/V protein.
PN   WO2003089451-A2.
PD   30-OCT-2003.
PA   (DYAX-) DYAX CORP.
  Query Match             6.9%;  Score 75.5;  DB 7;  Length 240;
  Best Local Similarity   24.2%;  Pred. No. 15;
RESULT 693
ID   ADI57768 standard; protein; 241 AA.
DE   Human breast specific protein (BSP) #45.
PN   WO2003106648-A2.
PD   24-DEC-2003.
PA   (DIAD-) DIADEXUS INC.
  Query Match             6.9%;  Score 75.5;  DB 8;  Length 241;
  Best Local Similarity   24.2%;  Pred. No. 15;
RESULT 694
ID   ADE48141 standard; protein; 249 AA.
DE   MUC1/V/alt protein.
PN   WO2003089451-A2.
PD   30-OCT-2003.
PA   (DYAX-) DYAX CORP.
  Query Match             6.9%;  Score 75.5;  DB 7;  Length 249;
  Best Local Similarity   24.2%;  Pred. No. 16;
RESULT 695
ID   AAR89420 standard; protein; 255 AA.
DE   Mucin-derived protein MUC1/Y.
PN   WO9603502-A2.
PD   08-FEB-1996.
PA   (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
  Query Match             6.9%;  Score 75.5;  DB 2;  Length 255;
  Best Local Similarity   24.2%;  Pred. No. 16;
RESULT 696
ID   ADA50573 standard; protein; 255 AA.
DE   Mucin 1 (MUC-1) splice variant #2 (MUC1Y), SEQ ID NO:28.
PN   WO2003031569-A2.
PD   17-APR-2003.
PA   (CENZ ) CENTOCOR INC.
  Query Match             6.9%;  Score 75.5;  DB 6;  Length 255;
  Best Local Similarity   24.2%;  Pred. No. 16;
RESULT 697
ID   ADE48138 standard; protein; 255 AA.
DE   MUC1/Y protein.
PN   WO2003089451-A2.
PD   30-OCT-2003.
PA   (DYAX-) DYAX CORP.
  Query Match             6.9%;  Score 75.5;  DB 7;  Length 255;
  Best Local Similarity   24.2%;  Pred. No. 16;
RESULT 698
ID   ADI57772 standard; protein; 255 AA.
DE   Human breast specific protein (BSP) #49.
PN   WO2003106648-A2.
PD   24-DEC-2003.
PA   (DIAD-) DIADEXUS INC.
  Query Match             6.9%;  Score 75.5;  DB 8;  Length 255;
  Best Local Similarity   24.2%;  Pred. No. 16;
RESULT 699
ID   AAR89421 standard; protein; 264 AA.
DE   Mucin-derived protein MUC1/Y/alt.
PN   WO9603502-A2.
PD   08-FEB-1996.
PA   (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
  Query Match             6.9%;  Score 75.5;  DB 2;  Length 264;
  Best Local Similarity   24.2%;  Pred. No. 17;
RESULT 700
ID   ADE48139 standard; protein; 264 AA.
DE   MUC1/Y/alt protein.
PN   WO2003089451-A2.
PD   30-OCT-2003.
PA   (DYAX-) DYAX CORP.
  Query Match             6.9%;  Score 75.5;  DB 7;  Length 264;
  Best Local Similarity   24.2%;  Pred. No. 17;
RESULT 701
ID   ADI57767 standard; protein; 264 AA.
DE   Human breast specific protein (BSP) #44.
PN   WO2003106648-A2.
PD   24-DEC-2003.
PA   (DIAD-) DIADEXUS INC.
  Query Match             6.9%;  Score 75.5;  DB 8;  Length 264;
  Best Local Similarity   24.2%;  Pred. No. 17;
RESULT 702
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ID AAR89418 standard; protein; 273 AA.
DE Mucin-derived protein MUC1/X.
PN WO9603502-A2.
PD 08-FEB-1996.
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
Query Match 6.9%; Score 75.5; DB 2; Length 273;
Best Local Similarity 24.2%; Pred. No. 18;
RESULT 703
ID ADE48136 standard; protein; 273 AA.
DE MUC1/X protein.
PN WO2003089451-A2.
PD 30-OCT-2003.
PA (DYAX-) DYAX CORP.
Query Match 6.9%; Score 75.5; DB 7; Length 273;
Best Local Similarity 24.2%; Pred. No. 18;
RESULT 704
ID ADI57753 standard; protein; 273 AA.
DE Human breast specific protein (BSP) #30.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 273;
Best Local Similarity 24.2%; Pred. No. 18;
RESULT 705
ID AAR89419 standard; protein; 282 AA.
DE Mucin-derived protein MUC1/X/alt.
PN WO9603502-A2.
PD 08-FEB-1996.
PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.
Query Match 6.9%; Score 75.5; DB 2; Length 282;
Best Local Similarity 24.2%; Pred. No. 19;
RESULT 706
ID ADE48137 standard; protein; 282 AA.
DE MUC1/X/alt protein.
PN WO2003089451-A2.
PD 30-OCT-2003.
PA (DYAX-) DYAX CORP.
Query Match 6.9%; Score 75.5; DB 7; Length 282;
Best Local Similarity 24.2%; Pred. No. 19;
RESULT 707
ID ABP68583 standard; protein; 299 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:281.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 299;
Best Local Similarity 21.6%; Pred. No. 20;
RESULT 708
ID ABP68445 standard; protein; 299 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:49.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 299;
Best Local Similarity 21.6%; Pred. No. 20;
RESULT 709
ID ADM18684 standard; protein; 299 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:49.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 299;
Best Local Similarity 21.6%; Pred. No. 20;
RESULT 710
ID ADM18916 standard; protein; 299 AA.
DE Rabbit B7-1 protein SEQ ID NO:281.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 299;
Best Local Similarity 21.6%; Pred. No. 20;
RESULT 711
ID ABP68509 standard; protein; 301 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:192.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 301;
Best Local Similarity 23.4%; Pred. No. 21;
RESULT 712
ID ADM18827 standard; protein; 301 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:192.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 301;
Best Local Similarity 23.4%; Pred. No. 21;
RESULT 713
ID ABP68512 standard; protein; 302 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:195.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 714
ID ABP68536 standard; protein; 302 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:219.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 715
ID ABP68458 standard; protein; 302 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:62.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 716
ID ABP68530 standard; protein; 302 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:213.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 717
ID ABP68497 standard; protein; 302 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:180.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 718
ID ABP68520 standard; protein; 302 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:203.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 719
ID ADM18848 standard; protein; 302 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:213.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 720
ID ADM18854 standard; protein; 302 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:219.

PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 721
ID ADM18830 standard; protein; 302 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:195.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 722
ID ADM18697 standard; protein; 302 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:62.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 723
ID ADM18815 standard; protein; 302 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:180.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 724
ID ADM18838 standard; protein; 302 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:203.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 302;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 725
ID ABP68521 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:204.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 303;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 726
ID ABP68528 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:211.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 5; Length 303;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 727
ID ADM18839 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:204.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 303;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 728
ID ADM18846 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:211.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 303;
Best Local Similarity 21.6%; Pred. No. 21;
RESULT 729
ID AAU84810 standard; protein; 312 AA.
DE Human MUC1R consensus sequence.
PN WO200190197-A1.
PD 29-NOV-2001.
PA (AUSU) UNIV AUSTRALIAN NAT.
Query Match 6.9%; Score 75.5; DB 5; Length 312;
Best Local Similarity 24.2%; Pred. No. 22;
RESULT 730
ID AAB43416 standard; protein; 321 AA.
DE Human cancer associated protein sequence SEQ ID NO:861.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 75.5; DB 3; Length 321;
Best Local Similarity 24.2%; Pred. No. 23;
RESULT 731
ID AAR96298 standard; peptide; 327 AA.
DE Glycoprotein 39 C terminal fragment.
PN JP07051065-A.
PD 28-FEB-1995.
PA (NIKO-) NIPPON KOTAI KENKYUSHO KK.
PA (UYKA-) UNIV KAGOSHIMA.
Query Match 6.9%; Score 75.5; DB 2; Length 327;
Best Local Similarity 24.2%; Pred. No. 23;
RESULT 732
ID ADP24569 standard; protein; 335 AA.
DE PRO polypeptide SEQ ID NO:1747.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.9%; Score 75.5; DB 8; Length 335;
Best Local Similarity 23.0%; Pred. No. 24;
RESULT 733
ID AAR27662 standard; protein; 348 AA.
DE C-terminal region of H23-ETA-T antigen.
PN WO9207000-A1.
PD 30-APR-1992.
PA (TRGE) TRANSGENE SA.
Query Match 6.9%; Score 75.5; DB 2; Length 348;
Best Local Similarity 24.2%; Pred. No. 25;
RESULT 734
ID ADJ34832 standard; protein; 378 AA.
DE Xylanase from an environmental sample seq id 48.
PN WO2003106654-A2.
PD 24-DEC-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 6.9%; Score 75.5; DB 8; Length 378;
Best Local Similarity 20.1%; Pred. No. 28;
RESULT 735
ID ADE43994 standard; protein; 381 AA.
DE Plasmid JNW389 gutted MUC-1 protein.
PN WO2003099193-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 381;
Best Local Similarity 24.2%; Pred. No. 29;
RESULT 736
ID ADI57770 standard; protein; 420 AA.
DE Human breast specific protein (BSP) #47.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 420;
Best Local Similarity 24.2%; Pred. No. 33;
RESULT 737
ID ADI57752 standard; protein; 435 AA.
DE Human breast specific protein (BSP) #29.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 435;
Best Local Similarity 24.2%; Pred. No. 35;
RESULT 738
ID AAR23973 standard; protein; 455 AA.
DE Transmembrane form of H23-ETA antigen.
PN WO9207000-A1.

PD 30-APR-1992.
PA (TRGE) TRANSGENE SA.
Query Match 6.9%; Score 75.5; DB 2; Length 455;
Best Local Similarity 24.2%; Pred. No. 37;
RESULT 739
ID AAY71024 standard; protein; 455 AA.
DE Human Mucin 1 (MUC-1) protein fragment #5.
PN WO200025827-A2.
PD 11-MAY-2000.
PA (MENA) MENARINI RICERCHE SPA.
Query Match 6.9%; Score 75.5; DB 3; Length 455;
Best Local Similarity 24.2%; Pred. No. 37;
RESULT 740
ID ADE43996 standard; protein; 461 AA.
DE Plasmid JNW399 MUC-1 protein.
PN WO2003099193-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 461;
Best Local Similarity 24.2%; Pred. No. 38;
RESULT 741
ID ADI57750 standard; protein; 463 AA.
DE Human breast specific protein (BSP) #27.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 463;
Best Local Similarity 24.2%; Pred. No. 38;
RESULT 742
ID AAE09508 standard; protein; 473 AA.
DE Human mucin-1 (MUC-1) protein.
PN WO200157068-A1.
PD 09-AUG-2001.
PA (AUST-) AUSTIN RES INST.
Query Match 6.9%; Score 75.5; DB 4; Length 473;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 743
ID AAU00573 standard; protein; 475 AA.
DE Human MUC1 polypeptide variant.
PN WO200118035-A2.
PD 15-MAR-2001.
PA (TRGE) TRANSGENE SA.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 6.9%; Score 75.5; DB 4; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 744
ID ABB77476 standard; protein; 475 AA.
DE Human MUC1 SEQ ID NO 3.
PN WO200226765-A2.
PD 04-APR-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 6.9%; Score 75.5; DB 5; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 745
ID ADA50567 standard; protein; 475 AA.
DE Mucin 1 (MUC-1), SEQ ID NO:22.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Query Match 6.9%; Score 75.5; DB 6; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 746
ID AAE37800 standard; protein; 475 AA.
DE Human mucin 1 transmembrane variant, MUC1-VI protein.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 6.9%; Score 75.5; DB 6; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 747
ID ADD14120 standard; protein; 475 AA.
DE Human src biomarker polypeptide SEQ ID NO:309.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.9%; Score 75.5; DB 7; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 748
ID ADE48133 standard; protein; 475 AA.
DE MUC1 amino acid sequence.
PN WO2003089451-A2.
PD 30-OCT-2003.
PA (DYAX-) DYAX CORP.
Query Match 6.9%; Score 75.5; DB 7; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 749
ID ADE43992 standard; protein; 475 AA.
DE Plasmid JNW283 MUC-1 protein.
PN WO2003099193-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 750
ID ADF32626 standard; protein; 475 AA.
DE Plasmid JNW283 MUC-1 amino acid sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 751
ID ADI57746 standard; protein; 475 AA.
DE Human breast specific protein (BSP) #23.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 752
ID ADK70494 standard; protein; 475 AA.
DE Respiratory disease differentially expressed protein #60.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 6.9%; Score 75.5; DB 8; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 753
ID ADO28643 standard; protein; 475 AA.
DE Human MUC1 protein SEQ ID NO:72.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.9%; Score 75.5; DB 8; Length 475;
Best Local Similarity 24.2%; Pred. No. 39;
RESULT 754
ID ADF32628 standard; protein; 479 AA.
DE Plasmid JNW358 MUC-1 amino acid sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 479;
Best Local Similarity 24.2%; Pred. No. 40;
RESULT 755
ID ADI57761 standard; protein; 483 AA.
DE Human breast specific protein (BSP) #38.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 483;
Best Local Similarity 24.2%; Pred. No. 40;
RESULT 756
ID ADI57749 standard; protein; 484 AA.
DE Human breast specific protein (BSP) #26.
PN WO2003106648-A2.
PD 24-DEC-2003.

PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 484;
Best Local Similarity 24.2%; Pred. No. 40;
RESULT 757
ID ADI57771 standard; protein; 485 AA.
DE Human breast specific protein (BSP) #48.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 485;
Best Local Similarity 24.2%; Pred. No. 40;
RESULT 758
ID ADI57760 standard; protein; 492 AA.
DE Human breast specific protein (BSP) #37.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 492;
Best Local Similarity 24.2%; Pred. No. 41;
RESULT 759
ID AAU00539 standard; protein; 495 AA.
DE Human MUC1 polypeptide.
PN WO200118035-A2.
PD 15-MAR-2001.
PA (TRGE) TRANSGENE SA.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 6.9%; Score 75.5; DB 4; Length 495;
Best Local Similarity 24.2%; Pred. No. 41;
RESULT 760
ID ADF32632 standard; protein; 495 AA.
DE Plasmid JNW321 2x VNTR MUC-1 amino acid sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 495;
Best Local Similarity 24.2%; Pred. No. 41;
RESULT 761
ID ABG96378 standard; protein; 515 AA.
DE Human ovarian cancer marker OV45.
PN WO200271928-A2.
PD 19-SEP-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.9%; Score 75.5; DB 5; Length 515;
Best Local Similarity 24.2%; Pred. No. 44;
RESULT 762
ID ADA50565 standard; protein; 515 AA.
DE Human mucin 1 (MUC-1), SEQ ID NO:20.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Query Match 6.9%; Score 75.5; DB 6; Length 515;
Best Local Similarity 24.2%; Pred. No. 44;
RESULT 763
ID ABR92123 standard; protein; 515 AA.
DE Human cervical cancer cell marker protein SEQ ID NO:156.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.9%; Score 75.5; DB 6; Length 515;
Best Local Similarity 24.2%; Pred. No. 44;
RESULT 764
ID AAE37797 standard; protein; 515 AA.
DE Human mucin 1 transmembrane protein.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 6.9%; Score 75.5; DB 6; Length 515;
Best Local Similarity 24.2%; Pred. No. 44;
RESULT 765
ID ADI57743 standard; protein; 515 AA.
DE Human breast specific protein (BSP) #20.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 515;
Best Local Similarity 24.2%; Pred. No. 44;
RESULT 766
ID ADJ66746 standard; protein; 515 AA.
DE Human Muc1 protein amino acid sequence.
PN WO2004005470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
Query Match 6.9%; Score 75.5; DB 8; Length 515;
Best Local Similarity 24.2%; Pred. No. 44;
RESULT 767
ID ADI57773 standard; protein; 517 AA.
DE Human breast specific protein (BSP) #50.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 517;
Best Local Similarity 24.2%; Pred. No. 44;
RESULT 768
ID ADI57742 standard; protein; 524 AA.
DE Human breast specific protein (BSP) #19.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 524;
Best Local Similarity 24.2%; Pred. No. 45;
RESULT 769
ID ADI57751 standard; protein; 524 AA.
DE Human breast specific protein (BSP) #28.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 524;
Best Local Similarity 24.2%; Pred. No. 45;
RESULT 770
ID ABU14879 standard; protein; 549 AA.
DE Protein encoded by Prokaryotic essential gene #406.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.9%; Score 75.5; DB 6; Length 549;
Best Local Similarity 20.3%; Pred. No. 48;
RESULT 771
ID AAY71030 standard; protein; 577 AA.
DE Ubiquitin-E. coli LacI-human Mucin 1 fusion protein #5.
PN WO200025827-A2.
PD 11-MAY-2000.
PA (MENA) MENARINI RICERCHE SPA.
Query Match 6.9%; Score 75.5; DB 3; Length 577;
Best Local Similarity 24.2%; Pred. No. 51;
RESULT 772
ID ADF32630 standard; protein; 595 AA.
DE Plasmid JNW319 7x VNTR MUC-1 amino acid sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 595;
Best Local Similarity 24.2%; Pred. No. 54;
RESULT 773
ID ADF32634 standard; protein; 599 AA.
DE Plasmid JNW656 7x VNTR MUC-1 amino acid sequence.
PN WO2003100060-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 599;
Best Local Similarity 24.2%; Pred. No. 54;
RESULT 774
ID ADR89852 standard; protein; 599 AA.
DE Human mucin MUC-1 with 7x VNTR.
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.

Query Match 6.9%; Score 75.5; DB 8; Length 599;
Best Local Similarity 24.2%; Pred. No. 54;
RESULT 775
ID ADH10476 standard; protein; 656 AA.
DE Human MUC-1-CPC fusion protein.
PN WO2003104272-A1.
PD 18-DEC-2003.
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 656;
Best Local Similarity 24.2%; Pred. No. 61;
RESULT 776
ID ADH10478 standard; protein; 678 AA.
DE CPC-MUC-1 fusion protein.
PN WO2003104272-A1.
PD 18-DEC-2003.
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
PA (GLAX) GLAXO GROUP LTD.
Query Match 6.9%; Score 75.5; DB 8; Length 678;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 777
ID ADC95237 standard; protein; 944 AA.
DE E. faecium protein sequence SEQ ID 4864.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.9%; Score 75.5; DB 7; Length 944;
Best Local Similarity 21.3%; Pred. No. 1e+02;
RESULT 778
ID ABP56040 standard; peptide; 1255 AA.
DE MUC1 receptor (mucin 1 precursor) SEQ ID NO:10.
PN WO200256022-A2.
PD 18-JUL-2002.
PA (MINE-) MINERVA BIOTECHNOLOGIES CORP.
Query Match 6.9%; Score 75.5; DB 5; Length 1255;
Best Local Similarity 24.2%; Pred. No. 1.5e+02;
RESULT 779
ID ABB82568 standard; protein; 1255 AA.
DE MUC1/REP transmembrane protein.
PN WO200278598-A2.
PD 10-OCT-2002.
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
Query Match 6.9%; Score 75.5; DB 6; Length 1255;
Best Local Similarity 24.2%; Pred. No. 1.5e+02;
RESULT 780
ID ABR47537 standard; protein; 1255 AA.
DE Breast cancer associated protein sequence SEQ ID NO:311.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.9%; Score 75.5; DB 6; Length 1255;
Best Local Similarity 24.2%; Pred. No. 1.5e+02;
RESULT 781
ID ABR92124 standard; protein; 1255 AA.
DE Human cervical cancer cell marker protein SEQ ID NO:158.
PN WO2002101075-A2.
PD 19-DEC-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.9%; Score 75.5; DB 6; Length 1255;
Best Local Similarity 24.2%; Pred. No. 1.5e+02;
RESULT 782
ID ADD45111 standard; protein; 1255 AA.
DE Human Protein Q16615, SEQ ID NO 10544.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.9%; Score 75.5; DB 7; Length 1255;
Best Local Similarity 24.2%; Pred. No. 1.5e+02;
RESULT 783
ID ADE54622 standard; protein; 1255 AA.
DE Human Protein Q16615, SEQ ID NO 427.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.9%; Score 75.5; DB 7; Length 1255;
Best Local Similarity 24.2%; Pred. No. 1.5e+02;
RESULT 784
ID ADQ29694 standard; protein; 1255 AA.
DE Human colorectal cancer-associated protein #49.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 6.9%; Score 75.5; DB 8; Length 1255;
Best Local Similarity 24.2%; Pred. No. 1.5e+02;
RESULT 785
ID ADI57740 standard; protein; 1256 AA.
DE Human breast specific protein (BSP) #17.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.9%; Score 75.5; DB 8; Length 1256;
Best Local Similarity 24.2%; Pred. No. 1.5e+02;
RESULT 786
ID ABB65886 standard; protein; 1279 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24450.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 75.5; DB 4; Length 1279;
Best Local Similarity 24.0%; Pred. No. 1.6e+02;
RESULT 787
ID ABB70362 standard; protein; 1713 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37878.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 75.5; DB 4; Length 1713;
Best Local Similarity 24.1%; Pred. No. 2.4e+02;
RESULT 788
ID AAU38981 standard; protein; 1713 AA.
DE Drosophila G-protein coupled receptor, GCPR #59.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 75.5; DB 4; Length 1713;
Best Local Similarity 24.1%; Pred. No. 2.4e+02;
RESULT 789
ID ADC35925 standard; protein; 1713 AA.
DE Drosophila G protein coupled receptor seq id 61.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match 6.9%; Score 75.5; DB 7; Length 1713;
Best Local Similarity 24.1%; Pred. No. 2.4e+02;
RESULT 790
ID ABR33128 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1346.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 791
ID ABR33360 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1713.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 792
ID ABR33127 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1345.

PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 793
ID ABR33334 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1687.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 794
ID ABR33340 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1693.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 795
ID ABR33142 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1360.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 796
ID ABR33144 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1362.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 797
ID ABR33357 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1710.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 798
ID ABR33292 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1645.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 799
ID ABR33339 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1692.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 800
ID ABR33441 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1794.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.8%; Score 75; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.35;
RESULT 801
ID ADO29551 standard; protein; 343 AA.
DE Mouse GPCR MRGF, SEQ ID NO:653.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.8%; Score 75; DB 8; Length 343;
Best Local Similarity 20.9%; Pred. No. 28;
RESULT 802
ID ADS08193 standard; protein; 548 AA.
DE Staphylococcus epidermis polypeptide seqid 7488.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
Query Match 6.8%; Score 75; DB 8; Length 548;
Best Local Similarity 32.7%; Pred. No. 54;
RESULT 803
ID ABG06933 standard; protein; 562 AA.
DE Novel human diagnostic protein #6924.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.8%; Score 75; DB 4; Length 562;
Best Local Similarity 22.1%; Pred. No. 56;
RESULT 804
ID AAY81803 standard; protein; 1260 AA.
DE Wild type (C57BL/6J) murine mahogany protein sequence.
PN WO200005373-A2.
PD 03-FEB-2000.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.8%; Score 75; DB 3; Length 1260;
Best Local Similarity 19.6%; Pred. No. 1.7e+02;
RESULT 805
ID ADE58694 standard; protein; 1472 AA.
DE Rat Protein NP_033860, SEQ ID NO 4570.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.8%; Score 75; DB 7; Length 1472;
Best Local Similarity 19.6%; Pred. No. 2.2e+02;
RESULT 806
ID ABP56658 standard; protein; 204 AA.
DE Chimpanzee C68 adenovirus E3 22.3 kDa protein SEQ ID NO:23.
PN WO2003000851-A2.
PD 03-JAN-2003.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 6.8%; Score 74.5; DB 6; Length 204;
Best Local Similarity 18.1%; Pred. No. 15;
RESULT 807
ID AAU11389 standard; protein; 307 AA.
DE Human T2R71 (hT2R71) polypeptide.
PN WO200177676-A1.
PD 18-OCT-2001.
PA (SENO-) SENOMYX INC.
Query Match 6.8%; Score 74.5; DB 5; Length 307;
Best Local Similarity 23.7%; Pred. No. 27;
RESULT 808
ID ABP95935 standard; protein; 307 AA.
DE Human GPCR polypeptide SEQ ID NO 680.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.8%; Score 74.5; DB 5; Length 307;
Best Local Similarity 23.7%; Pred. No. 27;
RESULT 809
ID ADC86989 standard; protein; 307 AA.
DE Human GPCR protein SEQ ID NO:1442.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 6.8%; Score 74.5; DB 7; Length 307;
Best Local Similarity 23.7%; Pred. No. 27;
RESULT 810
ID ADR29250 standard; protein; 307 AA.

DE Taste receptor modulation-related human T2R71 protein sequence SeqID189.
PN WO2004069191-A2.
PD 19-AUG-2004.
PA (SENO-) SENOMYX INC.
Query Match 6.8%; Score 74.5; DB 8; Length 307;
Best Local Similarity 23.7%; Pred. No. 27;
RESULT 811
ID ADM33293 standard; protein; 307 AA.
DE Human bitter taste receptor TAS2R41 protein SEQ ID NO:7.
PN WO2004029087-A2.
PD 08-APR-2004.
PA (DEER-) DEUT INST ERNAEHRUNGSFORSCHUNG POTSDAM.
Query Match 6.8%; Score 74.5; DB 8; Length 307;
Best Local Similarity 23.7%; Pred. No. 27;
RESULT 812
ID ABB92523 standard; protein; 664 AA.
DE Herbicidally active polypeptide SEQ ID NO 1734.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.8%; Score 74.5; DB 5; Length 664;
Best Local Similarity 21.5%; Pred. No. 81;
RESULT 813
ID ABR33135 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1353.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 814
ID ABR33303 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1656.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 815
ID ABR33361 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1714.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 816
ID ABR33394 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1747.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 817
ID ABR33374 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1727.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 818
ID ABR33338 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1691.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 819
ID ABR33401 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1754.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 820
ID ABR33091 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1309.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 821
ID ABR33134 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1352.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 822
ID ABR33417 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1770.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 823
ID ABR33356 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1709.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 824
ID ABR33110 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1328.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 825
ID ABR33396 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1749.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 826
ID ABR33426 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1779.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 827
ID ABR33320 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1673.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 828
ID ABR33308 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1661.
PN WO200283921-A2.

PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 829
ID ABR33293 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1646.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 830
ID ABR33333 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1686.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.7%; Score 74; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.46;
RESULT 831
ID ABP27051 standard; protein; 494 AA.
DE Streptococcus polypeptide SEQ ID NO 3278.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.7%; Score 74; DB 5; Length 494;
Best Local Similarity 23.3%; Pred. No. 61;
RESULT 832
ID ADS44884 standard; protein; 589 AA.
DE Bacterial polypeptide #23314.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 74; DB 8; Length 589;
Best Local Similarity 24.0%; Pred. No. 78;
RESULT 833
ID ADI57757 standard; protein; 614 AA.
DE Human breast specific protein (BSP) #34.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Query Match 6.7%; Score 74; DB 8; Length 614;
Best Local Similarity 22.5%; Pred. No. 82;
RESULT 834
ID ADH18889 standard; protein; 1005 AA.
DE Human cell adhesion and extracellular matrix CADECM-16 protein - SEQ 16.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 6.7%; Score 74; DB 8; Length 1005;
Best Local Similarity 28.6%; Pred. No. 1.6e+02;
RESULT 835
ID ABB58398 standard; protein; 154 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 1986.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 73.5; DB 4; Length 154;
Best Local Similarity 34.8%; Pred. No. 14;
RESULT 836
ID AAR48755 standard; protein; 298 AA.
DE Human thoracic aorta G-protein coupled receptor protein.
PN WO9405695-A1.
PD 17-MAR-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 6.7%; Score 73.5; DB 2; Length 298;
Best Local Similarity 21.0%; Pred. No. 34;
RESULT 837
ID AAW02727 standard; peptide; 298 AA.
DE Human thoracic aorta G-protein coupled receptor.
PN US5508384-A.
PD 16-APR-1996.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 6.7%; Score 73.5; DB 2; Length 298;
Best Local Similarity 21.0%; Pred. No. 34;
RESULT 838
ID ABP68446 standard; protein; 299 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:50.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.7%; Score 73.5; DB 5; Length 299;
Best Local Similarity 21.6%; Pred. No. 34;
RESULT 839
ID ADM18685 standard; protein; 299 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:50.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.7%; Score 73.5; DB 8; Length 299;
Best Local Similarity 21.6%; Pred. No. 34;
RESULT 840
ID ABP68505 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:188.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.7%; Score 73.5; DB 5; Length 303;
Best Local Similarity 21.6%; Pred. No. 35;
RESULT 841
ID ABP68517 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:200.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.7%; Score 73.5; DB 5; Length 303;
Best Local Similarity 21.6%; Pred. No. 35;
RESULT 842
ID ABP68518 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:201.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.7%; Score 73.5; DB 5; Length 303;
Best Local Similarity 21.6%; Pred. No. 35;
RESULT 843
ID ADM18835 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:200.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.7%; Score 73.5; DB 8; Length 303;
Best Local Similarity 21.6%; Pred. No. 35;
RESULT 844
ID ADM18836 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:201.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.7%; Score 73.5; DB 8; Length 303;
Best Local Similarity 21.6%; Pred. No. 35;
RESULT 845
ID ADM18823 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:188.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.7%; Score 73.5; DB 8; Length 303;
Best Local Similarity 21.6%; Pred. No. 35;
RESULT 846

ID ABB48941 standard; protein; 321 AA.
DE Listeria monocytogenes protein #1645.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.7%; Score 73.5; DB 5; Length 321;
Best Local Similarity 21.8%; Pred. No. 38;
RESULT 847
ID ABR53819 standard; protein; 465 AA.
DE Protein sequence #SEQ ID 2503.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 6.7%; Score 73.5; DB 6; Length 465;
Best Local Similarity 20.0%; Pred. No. 63;
RESULT 848
ID ADK65004 standard; protein; 465 AA.
DE Disease treating protein complex-derived protein #1514.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 6.7%; Score 73.5; DB 7; Length 465;
Best Local Similarity 20.0%; Pred. No. 63;
RESULT 849
ID ADN24173 standard; protein; 488 AA.
DE Bacterial polypeptide #6826.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 73.5; DB 8; Length 488;
Best Local Similarity 21.3%; Pred. No. 68;
RESULT 850
ID ADN26366 standard; protein; 498 AA.
DE Bacterial polypeptide #9019.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.7%; Score 73.5; DB 8; Length 498;
Best Local Similarity 19.2%; Pred. No. 70;
RESULT 851
ID ABU32150 standard; protein; 547 AA.
DE Protein encoded by Prokaryotic essential gene #17677.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 73.5; DB 6; Length 547;
Best Local Similarity 19.8%; Pred. No. 80;
RESULT 852
ID ABO62057 standard; protein; 562 AA.
DE Klebsiella pneumoniae polypeptide seqid 8574.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.7%; Score 73.5; DB 7; Length 562;
Best Local Similarity 19.8%; Pred. No. 83;
RESULT 853
ID ADD25508 standard; protein; 630 AA.
DE Binding domain-immunoglobulin fusion protein-associated protein #31.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENECRAFT INC.
Query Match 6.7%; Score 73.5; DB 7; Length 630;
Best Local Similarity 19.1%; Pred. No. 97;
RESULT 854
ID ADM26406 standard; protein; 656 AA.
DE Hyperthermophile Methanopyrus kandleri protein #1012.
PN WO2003076575-A2.
PD 18-SEP-2003.
PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
Query Match 6.7%; Score 73.5; DB 7; Length 656;
Best Local Similarity 23.8%; Pred. No. 1e+02;
RESULT 855
ID ABB97543 standard; protein; 785 AA.
DE Novel human protein SEQ ID NO: 811.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 73.5; DB 5; Length 785;
Best Local Similarity 18.6%; Pred. No. 1.3e+02;
RESULT 856
ID AAR49730 standard; protein; 796 AA.
DE Sequence encoded by murine OSF-4 cDNA.
PN EP585801-A2.
PD 09-MAR-1994.
PA (FARH) HOECHST JAPAN LTD.
Query Match 6.7%; Score 73.5; DB 2; Length 796;
Best Local Similarity 21.7%; Pred. No. 1.3e+02;
RESULT 857
ID AAB60418 standard; protein; 796 AA.
DE Mouse PrP-binding protein, OB-cadherin-1.
PN WO200100235-A1.
PD 04-JAN-2001.
PA (UYMC-) UNIV MCGILL.
PA (CAPR-) CAPRION PHARM INC.
Query Match 6.7%; Score 73.5; DB 4; Length 796;
Best Local Similarity 21.7%; Pred. No. 1.3e+02;
RESULT 858
ID ABB57294 standard; protein; 796 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:826.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 6.7%; Score 73.5; DB 5; Length 796;
Best Local Similarity 21.7%; Pred. No. 1.3e+02;
RESULT 859
ID ADI16949 standard; protein; 796 AA.
DE Murine NOVX protein homologue SeqID 485.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.7%; Score 73.5; DB 5; Length 796;
Best Local Similarity 21.7%; Pred. No. 1.3e+02;
RESULT 860
ID AAB18268 standard; protein; 1166 AA.
DE Plasmodium falciparum chromosome 2 related protein SEQ ID NO:125.
PN WO200025728-A2.
PD 11-MAY-2000.
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
Query Match 6.7%; Score 73.5; DB 3; Length 1166;
Best Local Similarity 22.1%; Pred. No. 2.3e+02;
RESULT 861
ID AAY04157 standard; peptide; 14 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:28.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 862
ID AAY11373 standard; protein; 14 AA.
DE Human 5' EST secreted protein SEQ ID NO:28.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.

Query Match 6.6%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 863
ID AAY04175 standard; peptide; 14 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:28.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 864
ID AAY12520 standard; peptide; 14 AA.
DE Human 5' EST signal peptide SEQ ID NO: 28 from WO 9906553.
PN WO9906553-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 865
ID AAY35891 standard; peptide; 14 AA.
DE Signal peptide of extended secreted protein, SEQ ID NO. 28.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 866
ID AAY59652 standard; peptide; 14 AA.
DE Secreted protein extended EST signal peptide #6.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 867
ID AAY25460 standard; peptide; 14 AA.
DE Human secreted protein 6 signal peptide derived from extended cDNA.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 868
ID AAY12679 standard; peptide; 14 AA.
DE Human 5' EST secreted protein signal peptide.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 869
ID AAY11715 standard; protein; 14 AA.
DE Peptide encoded by extended cDNA derived from 5' EST.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 870
ID AAY64646 standard; peptide; 14 AA.
DE Human 58-35-2-F10-FL2 signal peptide.
PN WO9953051-A2.
PD 21-OCT-1999.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 871
ID AAG00015 standard; peptide; 14 AA.
DE Human secreted protein #3 signal peptide.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 6.6%; Score 73; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 872
ID ADJ45875 standard; peptide; 14 AA.
DE Novel human secreted protein-related peptide sequence SeqID28.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 6.6%; Score 73; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 873
ID ADM77747 standard; peptide; 14 AA.
DE Signal sequence #6.
PN US2003162176-A1.
PD 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 6.6%; Score 73; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.54;
RESULT 874
ID ABR33399 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1752.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.6%; Score 73; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.59;
RESULT 875
ID ABR33407 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1760.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.6%; Score 73; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.59;
RESULT 876
ID ABR33446 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1799.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.6%; Score 73; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.59;
RESULT 877
ID ABR33366 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1719.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.6%; Score 73; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.59;
RESULT 878
ID ABR33409 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1762.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.6%; Score 73; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.59;
RESULT 879
ID ABR33085 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1303.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.6%; Score 73; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.59;
RESULT 880
ID ABR33094 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1312.
PN WO200283921-A2.

PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.6%; Score 73; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.59;
RESULT 881
ID ABR33349 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1702.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.6%; Score 73; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.59;
RESULT 882
ID ADF07700 standard; protein; 195 AA.
DE Bacterial polypeptide #3813.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.6%; Score 73; DB 7; Length 195;
Best Local Similarity 21.8%; Pred. No. 21;
RESULT 883
ID AAR85151 standard; protein; 205 AA.
DE Endothelial cell polypeptide.
PN EP682113-A2.
PD 15-NOV-1995.
PA (ONOY) ONO PHARM CO LTD.
Query Match 6.6%; Score 73; DB 2; Length 205;
Best Local Similarity 19.1%; Pred. No. 23;
RESULT 884
ID AAM78603 standard; protein; 205 AA.
DE Human protein SEQ ID NO 1265.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 73; DB 4; Length 205;
Best Local Similarity 19.1%; Pred. No. 23;
RESULT 885
ID ABR43432 standard; protein; 205 AA.
DE Human malignant neoplasm related protein SEQ ID NO:14.
PN WO2003025135-A2.
PD 27-MAR-2003.
PA (GENE-) GENE LOGIC INC.
Query Match 6.6%; Score 73; DB 6; Length 205;
Best Local Similarity 19.1%; Pred. No. 23;
RESULT 886
ID ADF61798 standard; protein; 205 AA.
DE Human D1-1 protein.
PN WO2003091447-A2.
PD 06-NOV-2003.
PA (CALY) CALIFORNIA INST OF TECHNOLOGY.
Query Match 6.6%; Score 73; DB 7; Length 205;
Best Local Similarity 19.1%; Pred. No. 23;
RESULT 887
ID ADE77093 standard; protein; 205 AA.
DE Human protein expressed in a liver disorder #68.
PN US2003108871-A1.
PD 12-JUN-2003.
PA (KASE/) KASER M R.
Query Match 6.6%; Score 73; DB 8; Length 205;
Best Local Similarity 19.1%; Pred. No. 23;
RESULT 888
ID AAB38322 standard; protein; 206 AA.
DE Human secreted protein encoded by gene 2 clone HEMFQ46.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 73; DB 3; Length 206;
Best Local Similarity 19.1%; Pred. No. 23;
RESULT 889
ID AAB58895 standard; protein; 221 AA.
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 603.
PN WO200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 73; DB 3; Length 221;
Best Local Similarity 19.1%; Pred. No. 25;
RESULT 890
ID AAM79587 standard; protein; 238 AA.
DE Human protein SEQ ID NO 3233.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 73; DB 4; Length 238;
Best Local Similarity 19.1%; Pred. No. 28;
RESULT 891
ID AAM79586 standard; protein; 238 AA.
DE Human protein SEQ ID NO 3232.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 73; DB 4; Length 238;
Best Local Similarity 19.1%; Pred. No. 28;
RESULT 892
ID ADN47010 standard; protein; 254 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID888.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.6%; Score 73; DB 8; Length 254;
Best Local Similarity 32.4%; Pred. No. 31;
RESULT 893
ID ADR99905 standard; protein; 272 AA.
DE Immune Response Associated Protein, IRAP-13, SEQ ID 13.
PN WO2004081197-A2.
PD 23-SEP-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 73; DB 8; Length 272;
Best Local Similarity 20.9%; Pred. No. 34;
RESULT 894
ID AAU75544 standard; protein; 370 AA.
DE Mouse B7-like protein, B7-L_m1.
PN WO200200710-A2.
PD 03-JAN-2002.
PA (AMGE-) AMGEN INC.
Query Match 6.6%; Score 73; DB 5; Length 370;
Best Local Similarity 22.4%; Pred. No. 52;
RESULT 895
ID ABU35478 standard; protein; 512 AA.
DE Protein encoded by Prokaryotic essential gene #21005.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.6%; Score 73; DB 6; Length 512;
Best Local Similarity 21.8%; Pred. No. 82;
RESULT 896
ID ABG29239 standard; protein; 979 AA.
DE Novel human diagnostic protein #29230.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.6%; Score 73; DB 4; Length 979;
Best Local Similarity 23.7%; Pred. No. 2e+02;
RESULT 897
ID ADD49069 standard; protein; 1147 AA.
DE Human NOV11a SEQ ID 42.
PN WO2003060149-A2.
PD 24-JUL-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.6%; Score 73; DB 7; Length 1147;
Best Local Similarity 23.7%; Pred. No. 2.5e+02;
RESULT 898
ID ADH71108 standard; protein; 1147 AA.
DE Human protein of the invention NOV2a SEQ ID NO:4.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.

Query Match 6.6%; Score 73; DB 8; Length 1147;
Best Local Similarity 23.7%; Pred. No. 2.5e+02;
RESULT 899
ID ABM83946 standard; protein; 1147 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4195.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 73; DB 8; Length 1147;
Best Local Similarity 23.7%; Pred. No. 2.5e+02;
RESULT 900
ID ABO84632 standard; protein; 1179 AA.
DE Human cancer-associated protein HP18-037.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.6%; Score 73; DB 8; Length 1179;
Best Local Similarity 23.7%; Pred. No. 2.6e+02;
RESULT 901
ID ABU03548 standard; protein; 1181 AA.
DE Angiogenesis-associated human protein sequence #93.
PN WO200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.6%; Score 73; DB 6; Length 1181;
Best Local Similarity 23.7%; Pred. No. 2.7e+02;
RESULT 902
ID ABR59703 standard; protein; 1181 AA.
DE Human VLA-2 receptor alpha 2 subunit.
PN WO2003029277-A2.
PD 10-APR-2003.
PA (RIGE-) RIGEL PHARM INC.
Query Match 6.6%; Score 73; DB 6; Length 1181;
Best Local Similarity 23.7%; Pred. No. 2.7e+02;
RESULT 903
ID AAG79775 standard; protein; 1181 AA.
DE Alpha2 integrin.
PN WO2002101070-A2.
PD 19-DEC-2002.
PA (RIGE-) RIGEL PHARM INC.
Query Match 6.6%; Score 73; DB 6; Length 1181;
Best Local Similarity 23.7%; Pred. No. 2.7e+02;
RESULT 904
ID ABU03616 standard; protein; 1181 AA.
DE Human expressed protein tag (EPT) #282.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.6%; Score 73; DB 6; Length 1181;
Best Local Similarity 23.7%; Pred. No. 2.7e+02;
RESULT 905
ID ABU03614 standard; protein; 1181 AA.
DE Human expressed protein tag (EPT) #280.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.6%; Score 73; DB 6; Length 1181;
Best Local Similarity 23.7%; Pred. No. 2.7e+02;
RESULT 906
ID ABU03617 standard; protein; 1181 AA.
DE Human expressed protein tag (EPT) #283.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.6%; Score 73; DB 6; Length 1181;
Best Local Similarity 23.7%; Pred. No. 2.7e+02;
RESULT 907
ID ADN39968 standard; protein; 1181 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C338.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.6%; Score 73; DB 7; Length 1181;
Best Local Similarity 23.7%; Pred. No. 2.7e+02;
RESULT 908
ID ABO84633 standard; protein; 1181 AA.
DE Human cancer-associated protein HP18-037.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.6%; Score 73; DB 8; Length 1181;
Best Local Similarity 23.7%; Pred. No. 2.7e+02;
RESULT 909
ID ADR46664 standard; protein; 1181 AA.
DE Cancer-associated protein, SEQ ID 77.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.6%; Score 73; DB 8; Length 1181;
Best Local Similarity 23.7%; Pred. No. 2.7e+02;
RESULT 910
ID ADN22950 standard; protein; 231 AA.
DE Bacterial polypeptide #5603.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.6%; Score 72.5; DB 8; Length 231;
Best Local Similarity 22.4%; Pred. No. 31;
RESULT 911
ID ADA50577 standard; protein; 252 AA.
DE Mucin 1 (MUC-1) splice variant #4 (MUC1Y variant), SEQ ID NO:32.
PN WO2003031569-A2.
PD 17-APR-2003.
PA (CENZ) CENTOCOR INC.
Query Match 6.6%; Score 72.5; DB 6; Length 252;
Best Local Similarity 23.1%; Pred. No. 35;
RESULT 912
ID AAE37798 standard; protein; 252 AA.
DE Human mucin 1 transmembrane variant, MUC1/Y protein.
PN WO2003054154-A2.
PD 03-JUL-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 6.6%; Score 72.5; DB 6; Length 252;
Best Local Similarity 23.1%; Pred. No. 35;
RESULT 913
ID ABP68579 standard; protein; 302 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:272.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 5; Length 302;
Best Local Similarity 21.6%; Pred. No. 45;
RESULT 914
ID ADM18907 standard; protein; 302 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:272.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 8; Length 302;
Best Local Similarity 21.6%; Pred. No. 45;
RESULT 915
ID ABP68457 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:61.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 916
ID ABP68502 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:185.
PN WO200200717-A2.

PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 917
ID ABP68585 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:283.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 918
ID ABP68510 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:193.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 919
ID ABP68503 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:186.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 920
ID ABP68514 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:197.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 921
ID ADM18918 standard; protein; 303 AA.
DE Co-stimulatory molecule consensus CD28BP protein SEQ ID NO:283.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 922
ID ADM18821 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:186.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 923
ID ADM18820 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:185.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 924
ID ADM18828 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:193.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 925
ID ADM18832 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:197.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 926
ID ADM18696 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:61.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.6%; Score 72.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 45;
RESULT 927
ID ABB92521 standard; protein; 682 AA.
DE Herbicidally active polypeptide SEQ ID NO 1732.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.6%; Score 72.5; DB 5; Length 682;
Best Local Similarity 23.7%; Pred. No. 1.4e+02;
RESULT 928
ID ABM69149 standard; protein; 912 AA.
DE Photorhabdus luminescens protein sequence #2246.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.6%; Score 72.5; DB 6; Length 912;
Best Local Similarity 22.1%; Pred. No. 2.1e+02;
RESULT 929
ID ABR33121 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1339.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 72; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.76;
RESULT 930
ID ABR33133 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1351.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 72; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.76;
RESULT 931
ID ABR33376 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1729.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 72; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.76;
RESULT 932
ID ABR33423 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1776.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 72; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.76;
RESULT 933
ID ABR33088 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1306.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 72; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.76;
RESULT 934
ID AAB74745 standard; protein; 157 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:54.
PN WO200112775-A2.
PD 22-FEB-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 72; DB 4; Length 157;
Best Local Similarity 22.3%; Pred. No. 20;
RESULT 935
ID ABG65312 standard; protein; 157 AA.
DE Human albumin fusion protein #1987.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 72; DB 5; Length 157;
Best Local Similarity 22.3%; Pred. No. 20;
RESULT 936
ID ADL78579 standard; protein; 157 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 2061.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 6.5%; Score 72; DB 8; Length 157;
Best Local Similarity 22.3%; Pred. No. 20;
RESULT 937
ID AAB74768 standard; protein; 185 AA.
DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:77.
PN WO200112775-A2.
PD 22-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 72; DB 4; Length 185;
Best Local Similarity 22.3%; Pred. No. 26;
RESULT 938
ID ADS85091 standard; protein; 293 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID93.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.
Query Match 6.5%; Score 72; DB 8; Length 293;
Best Local Similarity 20.0%; Pred. No. 49;
RESULT 939
ID ADL04462 standard; protein; 510 AA.
DE M. catarrhalis protein #228.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.5%; Score 72; DB 8; Length 510;
Best Local Similarity 19.6%; Pred. No. 1.1e+02;
RESULT 940
ID ABB71280 standard; protein; 588 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40632.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.5%; Score 72; DB 4; Length 588;
Best Local Similarity 25.8%; Pred. No. 1.3e+02;
RESULT 941
ID AAY28806 standard; protein; 653 AA.
DE cc359_4 secreted protein.
PN WO9950405-A1.
PD 07-OCT-1999.
PA (GEMY) GENETICS INST INC.
Query Match 6.5%; Score 72; DB 2; Length 653;
Best Local Similarity 20.3%; Pred. No. 1.5e+02;
RESULT 942
ID ADI16947 standard; protein; 792 AA.
DE Human NOVX protein homologue SeqID 483.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 72; DB 5; Length 792;
Best Local Similarity 19.1%; Pred. No. 2e+02;
RESULT 943
ID ADD46435 standard; protein; 1106 AA.
DE Rat Protein Q63258, SEQ ID NO 12115.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.5%; Score 72; DB 7; Length 1106;
Best Local Similarity 22.6%; Pred. No. 3.1e+02;
RESULT 944
ID ADN22331 standard; protein; 1447 AA.
DE Bacterial polypeptide #4984.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.5%; Score 72; DB 8; Length 1447;
Best Local Similarity 25.0%; Pred. No. 4.6e+02;
RESULT 945
ID ABU48947 standard; protein; 5005 AA.
DE Protein encoded by Prokaryotic essential gene #34474.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 72; DB 6; Length 5005;
Best Local Similarity 24.0%; Pred. No. 2.6e+03;
RESULT 946
ID ABP68524 standard; protein; 300 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:207.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 300;
Best Local Similarity 24.6%; Pred. No. 57;
RESULT 947
ID ABP68461 standard; protein; 300 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:65.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 300;
Best Local Similarity 24.6%; Pred. No. 57;
RESULT 948
ID ADM18842 standard; protein; 300 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:207.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 300;
Best Local Similarity 24.6%; Pred. No. 57;
RESULT 949
ID ADM18700 standard; protein; 300 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:65.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 300;
Best Local Similarity 24.6%; Pred. No. 57;
RESULT 950
ID ABP68462 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:66.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 951
ID ABP68519 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:202.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;

RESULT 952
ID ABP68534 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:217.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 953
ID ABP68498 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:181.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 954
ID ABP68463 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:67.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 955
ID ABP68459 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:63.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 956
ID ABP68504 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:187.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 957
ID ABP68506 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:189.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 958
ID ABP68526 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:209.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 959
ID ABP68451 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:55.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 960
ID ABP68454 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:58.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 961
ID ABP68456 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:60.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 962
ID ABP68453 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:57.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 963
ID ABP68448 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:52.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 964
ID ABP68447 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:51.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 965
ID ABP68511 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:194.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 966
ID ABP68522 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:205.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 967
ID ABP68525 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:208.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 968
ID ABP68452 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:56.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 969
ID ABP68450 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:54.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 970
ID ABP68496 standard; protein; 303 AA.

DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:179.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 971
ID ADM18814 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:179.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 972
ID ADM18829 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:194.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 973
ID ADM18701 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:66.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 974
ID ADM18824 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:189.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 975
ID ADM18816 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:181.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 976
ID ADM18840 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:205.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 977
ID ADM18698 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:63.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 978
ID ADM18844 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:209.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 979
ID ADM18693 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:58.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 980
ID ADM18702 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:67.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 981
ID ADM18837 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:202.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 982
ID ADM18687 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:52.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 983
ID ADM18843 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:208.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 984
ID ADM18690 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:55.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 985
ID ADM18686 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:51.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 986
ID ADM18689 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:54.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 987
ID ADM18691 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:56.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 988
ID ADM18692 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:57.
PN WO2004029197-A2.

PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 989
ID ADM18822 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:187.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 990
ID ADM18695 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:60.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 991
ID ADM18852 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:217.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.5%; Score 71.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 58;
RESULT 992
ID ABB47969 standard; protein; 331 AA.
DE Listeria monocytogenes protein #673.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.5%; Score 71.5; DB 5; Length 331;
Best Local Similarity 22.1%; Pred. No. 66;
RESULT 993
ID AAB88327 standard; protein; 348 AA.
DE Human membrane or secretory protein clone PSEC0028.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.5%; Score 71.5; DB 4; Length 348;
Best Local Similarity 21.7%; Pred. No. 71;
RESULT 994
ID ABU50797 standard; protein; 397 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #140.
PN WO200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP) INST PASTEUR.
Query Match 6.5%; Score 71.5; DB 5; Length 397;
Best Local Similarity 18.7%; Pred. No. 85;
RESULT 995
ID ADP99057 standard; protein; 450 AA.
DE C. albicans specific gene, orf19.3956, protein sequence.
PN WO2004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 6.5%; Score 71.5; DB 8; Length 450;
Best Local Similarity 27.6%; Pred. No. 1e+02;
RESULT 996
ID AAY36758 standard; protein; 453 AA.
DE Chlamydia trachomatis transport protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 6.5%; Score 71.5; DB 2; Length 453;
Best Local Similarity 24.6%; Pred. No. 1e+02;
RESULT 997
ID AAW77233 standard; protein; 508 AA.
DE MiniMUC1 protein.
PN WO9837095-A2.
PD 27-AUG-1998.
PA (THER-) THERION BIOLOGICS CORP.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 6.5%; Score 71.5; DB 2; Length 508;
Best Local Similarity 23.1%; Pred. No. 1.2e+02;
RESULT 998
ID AAM41006 standard; protein; 522 AA.
DE Human polypeptide SEQ ID NO 5937.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.5%; Score 71.5; DB 4; Length 522;
Best Local Similarity 21.8%; Pred. No. 1.2e+02;
RESULT 999
ID AAG63982 standard; protein; 549 AA.
DE Amino acid sequence of murine nectin-3.
PN WO200166736-A1.
PD 13-SEP-2001.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (TAKA/) TAKAHASHI K.
Query Match 6.5%; Score 71.5; DB 4; Length 549;
Best Local Similarity 25.3%; Pred. No. 1.3e+02;
RESULT 1000
ID AAG63985 standard; protein; 549 AA.
DE Amino acid sequence of murine nectin-3.
PN WO200166736-A1.
PD 13-SEP-2001.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (TAKA/) TAKAHASHI K.
Query Match 6.5%; Score 71.5; DB 4; Length 549;
Best Local Similarity 25.3%; Pred. No. 1.3e+02;
RESULT 1001
ID AAE23291 standard; protein; 549 AA.
DE Mouse nectin-3alpha protein.
PN WO200228902-A2.
PD 11-APR-2002.
PA (IMMV) IMMUNEX CORP.
Query Match 6.5%; Score 71.5; DB 5; Length 549;
Best Local Similarity 25.3%; Pred. No. 1.3e+02;
RESULT 1002
ID ABM84085 standard; protein; 559 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4334.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.5%; Score 71.5; DB 8; Length 559;
Best Local Similarity 30.6%; Pred. No. 1.4e+02;
RESULT 1003
ID AAG30391 standard; protein; 668 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36324.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 71.5; DB 3; Length 668;
Best Local Similarity 24.7%; Pred. No. 1.8e+02;
RESULT 1004
ID AAG30390 standard; protein; 692 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36323.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.5%; Score 71.5; DB 3; Length 692;
Best Local Similarity 24.7%; Pred. No. 1.8e+02;
RESULT 1005
ID ABB93188 standard; protein; 692 AA.
DE Herbicidally active polypeptide SEQ ID NO 2399.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.5%; Score 71.5; DB 5; Length 692;
Best Local Similarity 24.7%; Pred. No. 1.8e+02;
RESULT 1006
ID ABB58214 standard; protein; 713 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 1434.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.5%; Score 71.5; DB 4; Length 713;
Best Local Similarity 24.5%; Pred. No. 1.9e+02;
RESULT 1007
ID ABB93899 standard; protein; 718 AA.
DE Herbicidally active polypeptide SEQ ID NO 3110.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.5%; Score 71.5; DB 5; Length 718;
Best Local Similarity 23.0%; Pred. No. 1.9e+02;
RESULT 1008
ID AAR49731 standard; protein; 796 AA.
DE Sequence encoded by human OSF-4-1 cDNA.
PN EP585801-A2.
PD 09-MAR-1994.
PA (FARH) HOECHST JAPAN LTD.
Query Match 6.5%; Score 71.5; DB 2; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1009
ID AAW25636 standard; protein; 796 AA.
DE Human cadherin-11.
PN US5646250-A.
PD 08-JUL-1997.
PA (DOHE-) DOHENY EYE INST.
Query Match 6.5%; Score 71.5; DB 2; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1010
ID AAW13134 standard; protein; 796 AA.
DE Full length human cadherin-11.
PN US5597725-A.
PD 28-JAN-1997.
PA (DOHE-) DOHENY EYE INST.
Query Match 6.5%; Score 71.5; DB 2; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1011
ID AAW85598 standard; protein; 796 AA.
DE Cadherin-11.
PN WO9849560-A1.
PD 05-NOV-1998.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Query Match 6.5%; Score 71.5; DB 2; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1012
ID AAB60419 standard; protein; 796 AA.
DE Human PrP-binding protein, OB-cadherin-1 (cadherin-11).
PN WO200100235-A1.
PD 04-JAN-2001.
PA (UYMC-) UNIV MCGILL.
PA (CAPR-) CAPRION PHARM INC.
Query Match 6.5%; Score 71.5; DB 4; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1013
ID AAB67624 standard; protein; 796 AA.
DE Amino acid sequence of a human cadherin-11 polypeptide.
PN WO200117557-A1.
PD 15-MAR-2001.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 6.5%; Score 71.5; DB 4; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1014
ID ADI16950 standard; protein; 796 AA.
DE Human NOVX protein homologue SeqID 486.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 71.5; DB 5; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1015
ID ADP18662 standard; protein; 796 AA.
DE Human protein encoded by TAT400 cDNA used to treat cancer SeqID 22.
PN WO2004045516-A2.
PD 03-JUN-2004.
PA (GETH) GENENTECH INC.
Query Match 6.5%; Score 71.5; DB 8; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1016
ID ADP26903 standard; protein; 796 AA.
DE Human OB-cadherin protein SEQ ID NO:4.
PN EP1428893-A2.
PD 16-JUN-2004.
PA (SPRE/) SPRECHER E.
PA (BERG/) BERGMAN R.
Query Match 6.5%; Score 71.5; DB 8; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1017
ID ADR48218 standard; protein; 796 AA.
DE Human cadherin 11 type 2 OB-cadherin protein SEQ:6.
PN WO2004074510-A1.
PD 02-SEP-2004.
PA (GARV-) GARVAN INST MEDICAL RES.
Query Match 6.5%; Score 71.5; DB 8; Length 796;
Best Local Similarity 30.6%; Pred. No. 2.2e+02;
RESULT 1018
ID ABU30775 standard; protein; 936 AA.
DE Protein encoded by Prokaryotic essential gene #16302.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.5%; Score 71.5; DB 6; Length 936;
Best Local Similarity 18.7%; Pred. No. 2.8e+02;
RESULT 1019
ID ADN23173 standard; protein; 1139 AA.
DE Bacterial polypeptide #5826.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.5%; Score 71.5; DB 8; Length 1139;
Best Local Similarity 23.0%; Pred. No. 3.7e+02;
RESULT 1020
ID ABR33413 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1766.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1021
ID ABR33283 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1636.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1022
ID ABR33430 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1783.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1023
ID ABR33422 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1775.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.

Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1024
ID ABR33424 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1777.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1025
ID ABR33118 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1336.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1026
ID ABR33146 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1364.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1027
ID ABR33327 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1680.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1028
ID ABR33331 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1684.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1029
ID ABR33141 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1359.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1030
ID ABR33429 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1782.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1031
ID ABR33348 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1701.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1032
ID ABR33124 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1342.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1033
ID ABR33365 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1718.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1034
ID ABR33104 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1322.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1035
ID ABR33445 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1798.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1036
ID ABR33402 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1755.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1037
ID ABR33386 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1739.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1038
ID ABR33093 standard; peptide; 15 AA.
DE Human cancer-related protein 156P1D4 HLA peptide #1311.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1039
ID ABR33343 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1696.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 71; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.99;
RESULT 1040
ID AAG09853 standard; protein; 81 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 7946.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 71; DB 3; Length 81;
Best Local Similarity 27.9%; Pred. No. 10;
RESULT 1041
ID ABP69646 standard; protein; 183 AA.
DE Human polypeptide SEQ ID NO 1693.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 71; DB 5; Length 183;
Best Local Similarity 22.0%; Pred. No. 33;
RESULT 1042

ID ADA55095 standard; protein; 183 AA.
DE Human protein, SEQ ID 2663.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 71; DB 6; Length 183;
Best Local Similarity 22.0%; Pred. No. 33;
RESULT 1043
ID ADS74327 standard; protein; 183 AA.
DE PRO polypeptide PRO92173, role in immune-related disease.
PN WO2004081199-A2.
PD 23-SEP-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 183;
Best Local Similarity 22.0%; Pred. No. 33;
RESULT 1044
ID ABG15265 standard; protein; 234 AA.
DE Novel human diagnostic protein #15256.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 71; DB 4; Length 234;
Best Local Similarity 32.3%; Pred. No. 46;
RESULT 1045
ID ABB08196 standard; protein; 235 AA.
DE DPCR1 gene product within human leukocyte antigen (HLA) domain.
PN WO200248348-A1.
PD 20-JUN-2002.
PA (INOK/) INOKO H.
Query Match 6.4%; Score 71; DB 5; Length 235;
Best Local Similarity 18.3%; Pred. No. 46;
RESULT 1046
ID ADA84039 standard; protein; 235 AA.
DE Human DPCR1 protein.
PN WO2002103028-A2.
PD 27-DEC-2002.
PA (BIOM-) BIOMEDICAL CENT.
Query Match 6.4%; Score 71; DB 6; Length 235;
Best Local Similarity 18.3%; Pred. No. 46;
RESULT 1047
ID ADN39108 standard; protein; 235 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:426.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.4%; Score 71; DB 7; Length 235;
Best Local Similarity 18.3%; Pred. No. 46;
RESULT 1048
ID ADN39978 standard; protein; 235 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C348.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.4%; Score 71; DB 7; Length 235;
Best Local Similarity 18.3%; Pred. No. 46;
RESULT 1049
ID ADN39977 standard; protein; 235 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C347.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.4%; Score 71; DB 7; Length 235;
Best Local Similarity 18.3%; Pred. No. 46;
RESULT 1050
ID ADH18898 standard; protein; 330 AA.
DE Human cell adhesion and extracellular matrix CADECM-25 protein - SEQ 25.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 6.4%; Score 71; DB 8; Length 330;
Best Local Similarity 20.2%; Pred. No. 74;
RESULT 1051
ID ADO57299 standard; protein; 336 AA.
DE Kidney development associated protein seqid 66.
PN US2004068763-A1.
PD 08-APR-2004.
PA (HOPK/) HOPKINS N.
PA (GOLL/) GOLLING G.
PA (AMST/) AMSTERDAM A.
PA (SUNZ/) SUN Z.
Query Match 6.4%; Score 71; DB 8; Length 336;
Best Local Similarity 27.8%; Pred. No. 76;
RESULT 1052
ID ABU04649 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1315.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 338;
Best Local Similarity 20.2%; Pred. No. 77;
RESULT 1053
ID ABU04605 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1271.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 338;
Best Local Similarity 20.2%; Pred. No. 77;
RESULT 1054
ID AAR20816 standard; protein; 361 AA.
DE Haematopoietic CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 71; DB 2; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1055
ID AAR91444 standard; protein; 361 AA.
DE Human haematopoietic CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 71; DB 2; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1056
ID AAW80453 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 71; DB 2; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1057
ID AAW86200 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 71; DB 2; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1058
ID AAY99851 standard; protein; 361 AA.
DE Human CD44 cell surface adhesion receptor.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 6.4%; Score 71; DB 3; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1059
ID AAY96139 standard; protein; 361 AA.
DE Human haematopoietic CD44.5.
PN US6111093-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 71; DB 3; Length 361;

Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1060
ID AAU02448 standard; protein; 361 AA.
DE Human haematopoietic antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 71; DB 4; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1061
ID ABU04622 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1288.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1062
ID ABU04632 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1298.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1063
ID ABU04643 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1309.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1064
ID ABU04610 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1065
ID ABU04638 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1304.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1066
ID ABU04634 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1300.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1067
ID ABU04626 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1292.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1068
ID ABU04630 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1296.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1069
ID ABU04609 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1070
ID ABU04644 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1310.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1071
ID ABU04607 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1273.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1072
ID ABU04636 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1302.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1073
ID AAE30338 standard; protein; 361 AA.
DE Human CD44 antigen.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 6.4%; Score 71; DB 6; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1074
ID ADD90592 standard; protein; 361 AA.
DE Human CD44std glycoprotein SEQ ID NO:2.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 6.4%; Score 71; DB 7; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1075
ID ADO49373 standard; protein; 361 AA.
DE Human CD44 #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 6.4%; Score 71; DB 8; Length 361;
Best Local Similarity 20.2%; Pred. No. 84;
RESULT 1076
ID ADQ39385 standard; protein; 361 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 71; DB 8; Length 361;

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  Best Local Similarity   20.2%;  Pred. No. 84;
RESULT 1077
ID   ABU04615 standard; protein; 395 AA.
DE   Human expressed protein tag (EPT) #1281.
PN   WO200278524-A2.
PD   10-OCT-2002.
PA   (ZYCO-) ZYCOS INC.
  Query Match             6.4%;  Score 71;  DB 6;  Length 395;
  Best Local Similarity   20.2%;  Pred. No. 96;
RESULT 1078
ID   ADQ39389 standard; protein; 395 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1052.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
  Query Match             6.4%;  Score 71;  DB 8;  Length 395;
  Best Local Similarity   20.2%;  Pred. No. 96;
RESULT 1079
ID   ABU04617 standard; protein; 425 AA.
DE   Human expressed protein tag (EPT) #1283.
PN   WO200278524-A2.
PD   10-OCT-2002.
PA   (ZYCO-) ZYCOS INC.
  Query Match             6.4%;  Score 71;  DB 6;  Length 425;
  Best Local Similarity   20.2%;  Pred. No. 1.1e+02;
RESULT 1080
ID   ADQ39382 standard; protein; 425 AA.
DE   Human myocardial infarction-associated gene derived protein, SEQ ID 1045.
PN   WO2004058052-A2.
PD   15-JUL-2004.
PA   (APPL-) APPLERA CORP.
  Query Match             6.4%;  Score 71;  DB 8;  Length 425;
  Best Local Similarity   20.2%;  Pred. No. 1.1e+02;
RESULT 1081
ID   ABU04651 standard; protein; 470 AA.
DE   Human expressed protein tag (EPT) #1317.
PN   WO200278524-A2.
PD   10-OCT-2002.
PA   (ZYCO-) ZYCOS INC.
  Query Match             6.4%;  Score 71;  DB 6;  Length 470;
  Best Local Similarity   20.2%;  Pred. No. 1.2e+02;
RESULT 1082
ID   ABU04603 standard; protein; 470 AA.
DE   Human expressed protein tag (EPT) #1269.
PN   WO200278524-A2.
PD   10-OCT-2002.
PA   (ZYCO-) ZYCOS INC.
  Query Match             6.4%;  Score 71;  DB 6;  Length 470;
  Best Local Similarity   20.2%;  Pred. No. 1.2e+02;
RESULT 1083
ID   ABB49430 standard; protein; 489 AA.
DE   Listeria monocytogenes protein #2134.
PN   WO200177335-A2.
PD   18-OCT-2001.
PA   (INSP ) INST PASTEUR.
  Query Match             6.4%;  Score 71;  DB 5;  Length 489;
  Best Local Similarity   20.0%;  Pred. No. 1.3e+02;
RESULT 1084
ID   AAR20817 standard; protein; 493 AA.
DE   Epithelial CD44 Antigen.
PN   WO9201049-A.
PD   23-JAN-1992.
PA   (GEHO ) GEN HOSPITAL CORP.
  Query Match             6.4%;  Score 71;  DB 2;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1085
ID   AAR91445 standard; protein; 493 AA.
DE   Human epithelial CD44 antigen.
PN   US5506126-A.
PD   09-APR-1996.
PA   (GEHO ) GEN HOSPITAL CORP.
  Query Match             6.4%;  Score 71;  DB 2;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1086
ID   AAW80454 standard; protein; 493 AA.
DE   Human CD44 antigen (epithelial form).
PN   US5830731-A.
PD   03-NOV-1998.
PA   (GEHO ) GEN HOSPITAL CORP.
  Query Match             6.4%;  Score 71;  DB 2;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1087
ID   AAW89151 standard; protein; 493 AA.
DE   Human CD44 antigen (epithelial form).
PN   US5849898-A.
PD   15-DEC-1998.
PA   (GEHO ) GEN HOSPITAL CORP.
  Query Match             6.4%;  Score 71;  DB 2;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1088
ID   AAY96140 standard; protein; 493 AA.
DE   Human epithelial CD44.
PN   US6111093-A.
PD   29-AUG-2000.
PA   (GEHO ) GEN HOSPITAL CORP.
  Query Match             6.4%;  Score 71;  DB 3;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1089
ID   AAU02449 standard; protein; 493 AA.
DE   Human epithelial antigen CD44 polypeptide.
PN   US6218525-B1.
PD   17-APR-2001.
PA   (GEHO ) GEN HOSPITAL CORP.
  Query Match             6.4%;  Score 71;  DB 4;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1090
ID   AAU99123 standard; protein; 493 AA.
DE   Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.
PN   WO200244342-A2.
PD   06-JUN-2002.
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
  Query Match             6.4%;  Score 71;  DB 5;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1091
ID   ABU04637 standard; protein; 493 AA.
DE   Human expressed protein tag (EPT) #1303.
PN   WO200278524-A2.
PD   10-OCT-2002.
PA   (ZYCO-) ZYCOS INC.
  Query Match             6.4%;  Score 71;  DB 6;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1092
ID   ABU04627 standard; protein; 493 AA.
DE   Human expressed protein tag (EPT) #1293.
PN   WO200278524-A2.
PD   10-OCT-2002.
PA   (ZYCO-) ZYCOS INC.
  Query Match             6.4%;  Score 71;  DB 6;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1093
ID   ABU04639 standard; protein; 493 AA.
DE   Human expressed protein tag (EPT) #1305.
PN   WO200278524-A2.
PD   10-OCT-2002.
PA   (ZYCO-) ZYCOS INC.
  Query Match             6.4%;  Score 71;  DB 6;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1094
ID   ABU04623 standard; protein; 493 AA.
DE   Human expressed protein tag (EPT) #1289.
PN   WO200278524-A2.
PD   10-OCT-2002.
PA   (ZYCO-) ZYCOS INC.
  Query Match             6.4%;  Score 71;  DB 6;  Length 493;
  Best Local Similarity   20.2%;  Pred. No. 1.3e+02;
RESULT 1095
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ID ABU04631 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1297.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 493;
Best Local Similarity 20.2%; Pred. No. 1.3e+02;
RESULT 1096
ID ABU04633 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1299.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 493;
Best Local Similarity 20.2%; Pred. No. 1.3e+02;
RESULT 1097
ID ABU04612 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1278.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 493;
Best Local Similarity 20.2%; Pred. No. 1.3e+02;
RESULT 1098
ID ABU04635 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1301.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 493;
Best Local Similarity 20.2%; Pred. No. 1.3e+02;
RESULT 1099
ID ABU04613 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1279.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 493;
Best Local Similarity 20.2%; Pred. No. 1.3e+02;
RESULT 1100
ID ADL93507 standard; protein; 493 AA.
DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 6.4%; Score 71; DB 8; Length 493;
Best Local Similarity 20.2%; Pred. No. 1.3e+02;
RESULT 1101
ID ADO49375 standard; protein; 493 AA.
DE Human CD44 #2.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 6.4%; Score 71; DB 8; Length 493;
Best Local Similarity 20.2%; Pred. No. 1.3e+02;
RESULT 1102
ID ADQ39388 standard; protein; 493 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 71; DB 8; Length 493;
Best Local Similarity 20.2%; Pred. No. 1.3e+02;
RESULT 1103
ID ABB52510 standard; protein; 496 AA.
DE Escherichia coli polypeptide SEQ ID NO 370.
PN WO200166572-A2.
PD 13-SEP-2001.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 6.4%; Score 71; DB 4; Length 496;
Best Local Similarity 24.6%; Pred. No. 1.3e+02;
RESULT 1104
ID ABU40961 standard; protein; 496 AA.
DE Protein encoded by Prokaryotic essential gene #26488.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 71; DB 6; Length 496;
Best Local Similarity 23.1%; Pred. No. 1.3e+02;
RESULT 1105
ID AAM39220 standard; protein; 511 AA.
DE Human polypeptide SEQ ID NO 2365.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 71; DB 4; Length 511;
Best Local Similarity 21.1%; Pred. No. 1.4e+02;
RESULT 1106
ID ADE95616 standard; protein; 514 AA.
DE Human NOVX28a protein.
PN WO2003050245-A2.
PD 19-JUN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 71; DB 7; Length 514;
Best Local Similarity 23.0%; Pred. No. 1.4e+02;
RESULT 1107
ID ABM83594 standard; protein; 535 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.4%; Score 71; DB 8; Length 535;
Best Local Similarity 20.2%; Pred. No. 1.5e+02;
RESULT 1108
ID ADQ39381 standard; protein; 535 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 71; DB 8; Length 535;
Best Local Similarity 20.2%; Pred. No. 1.5e+02;
RESULT 1109
ID ADF06579 standard; protein; 542 AA.
DE Bacterial polypeptide #2692.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.4%; Score 71; DB 7; Length 542;
Best Local Similarity 23.1%; Pred. No. 1.5e+02;
RESULT 1110
ID AAW35382 standard; protein; 560 AA.
DE Murine metastatic nucleic acid sequence product.
PN WO9718454-A2.
PD 22-MAY-1997.
PA (THOM/) THOMPSON T.
Query Match 6.4%; Score 71; DB 2; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1111
ID AAB11329 standard; protein; 560 AA.
DE Human lung cancer-associated protein L528S.
PN WO200061612-A2.
PD 19-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match 6.4%; Score 71; DB 3; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1112
ID ABB78200 standard; protein; 560 AA.

DE Amino acid sequence of human HGFIN.
PN WO200262947-A2.
PD 15-AUG-2002.
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
Query Match 6.4%; Score 71; DB 5; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1113
ID ABB74961 standard; protein; 560 AA.
DE Human lung tumour L528S protein sequence SEQ ID NO:225.
PN WO200200174-A2.
PD 03-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 6.4%; Score 71; DB 5; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1114
ID ABP61881 standard; protein; 560 AA.
DE Human lung cancer associated protein sequence SEQ ID NO:225.
PN WO200247534-A2.
PD 20-JUN-2002.
PA (CORI-) CORIXA CORP.
Query Match 6.4%; Score 71; DB 5; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1115
ID ABU56592 standard; protein; 560 AA.
DE Lung cancer-associated polypeptide #185.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.4%; Score 71; DB 6; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1116
ID ABG72962 standard; protein; 560 AA.
DE Human osteoactivin homologue, nmb.
PN US2002151486-A1.
PD 17-OCT-2002.
PA (POPO/) POPOFF S N.
PA (SAFA/) SAFADI F F.
PA (OWEN/) OWEN T A.
PA (SMOC/) SMOCK S L.
Query Match 6.4%; Score 71; DB 6; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1117
ID ABU70852 standard; protein; 560 AA.
DE Human adipocyte Selected Interacting domain, SID, #483.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 6.4%; Score 71; DB 6; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1118
ID ADA28315 standard; protein; 560 AA.
DE Human lung tumour L528S protein.
PN US2003064947-A1.
PD 03-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.4%; Score 71; DB 7; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1119
ID ADE95620 standard; protein; 560 AA.
DE Human NOVX28c protein.
PN WO2003050245-A2.
PD 19-JUN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 71; DB 7; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1120
ID ADH36879 standard; protein; 560 AA.
DE Human lung cancer-related protein #16.
PN WO2003086175-A2.
PD 23-OCT-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.4%; Score 71; DB 7; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1121
ID ADJ68660 standard; protein; 560 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID466.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.4%; Score 71; DB 7; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1122
ID ADL14995 standard; protein; 560 AA.
DE Human NMB protein for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match 6.4%; Score 71; DB 7; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1123
ID ADN39940 standard; protein; 560 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C310.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.4%; Score 71; DB 7; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1124
ID ADH56342 standard; protein; 560 AA.
DE Human nmb protein SEQ ID NO:1.
PN WO2004002516-A1.
PD 08-JAN-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.4%; Score 71; DB 8; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1125
ID ADJ75569 standard; protein; 560 AA.
DE Marker gene related amino acid sequence SEQ ID NO:821.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 6.4%; Score 71; DB 8; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1126
ID ADM56682 standard; protein; 560 AA.
DE Human lung tumour polypeptide #16.
PN US2003138438-A1.
PD 24-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.4%; Score 71; DB 8; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1127
ID ADQ18310 standard; protein; 560 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1128.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.4%; Score 71; DB 8; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1128
ID ADP23127 standard; protein; 560 AA.
DE PRO polypeptide SEQ ID NO:221.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 560;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1129
ID ADR66659 standard; protein; 563 AA.
DE Human prostatic carcinoma derived protein SEQ ID 171 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 6.4%; Score 71; DB 8; Length 563;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1130
ID ADR66317 standard; protein; 563 AA.
DE Human prostatic carcinoma derived protein SEQ ID 171 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 6.4%; Score 71; DB 8; Length 563;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1131
ID ADR66339 standard; protein; 563 AA.
DE Human prostatic carcinoma derived protein SEQ ID 193 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 6.4%; Score 71; DB 8; Length 563;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1132
ID ADR66681 standard; protein; 563 AA.
DE Human prostatic carcinoma derived protein SEQ ID 193 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 6.4%; Score 71; DB 8; Length 563;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1133
ID AAU83612 standard; protein; 572 AA.
DE Human PRO protein, Seq ID No 42.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 5; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1134
ID ABU80759 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 6; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1135
ID ABO33725 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 6; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1136
ID ABU82068 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 6; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1137
ID ABJ72248 standard; protein; 572 AA.
DE Human PRO9925 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 6; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1138
ID ABJ72376 standard; protein; 572 AA.
DE Human PRO9925 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 6; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1139
ID ABO34271 standard; protein; 572 AA.
DE Human secreted/transmembrane polypeptide PRO 9925.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 6; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1140
ID ABJ72078 standard; protein; 572 AA.
DE Human membrane bound receptor/protein PRO9925 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1141
ID ADB83532 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1142
ID ADB80638 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1143
ID ADB73179 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1144
ID ADB78261 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1145
ID ADB84909 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1146
ID ADB78015 standard; protein; 572 AA.

DE Novel human secreted and transmembrane protein PRO9925.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1147
ID ADB87081 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1148
ID ADB84663 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1149
ID ADB83778 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1150
ID ADB72933 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1151
ID ADC36771 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1152
ID ADC21761 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1153
ID ADC49792 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1154
ID ADC48991 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1155
ID ADC49508 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1156
ID ADC47369 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1157
ID ADC47114 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1158
ID ADC77989 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1159
ID ADD06224 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1160
ID ADC77743 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1161
ID ADD50706 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1162
ID ADD50952 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1163
ID ADD50433 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1164
ID ADD50187 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003096970-A1.

PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1165
ID ADD51198 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1166
ID ADD78235 standard; protein; 572 AA.
DE Human CGDD-16.
PN WO2003077875-A2.
PD 25-SEP-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 71; DB 7; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1167
ID ADC48745 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1168
ID ADE20916 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1169
ID ADE05760 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1170
ID ADD74989 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1171
ID ADD75735 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1172
ID ADD84967 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1173
ID ADD86793 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1174
ID ADE20670 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1175
ID ADE38967 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1176
ID ADE05514 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1177
ID ADD73499 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1178
ID ADD78339 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1179
ID ADE21162 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1180
ID ADD77277 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1181
ID ADE20424 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1182
ID ADD75489 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1183
ID ADD74005 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1184
ID ADD74251 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1185
ID ADD75981 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1186
ID ADD85473 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1187
ID ADE05022 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1188
ID ADD75235 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1189
ID ADD76779 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1190
ID ADD86547 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1191
ID ADD78015 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1192
ID ADD77523 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1193
ID ADD77769 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1194
ID ADD85227 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1195
ID ADD73759 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1196
ID ADD74497 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1197
ID ADD77025 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1198
ID ADD85719 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1199
ID ADE05268 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1200
ID ADD74743 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;

RESULT 1201
ID ADG05555 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1202
ID ADG27109 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1203
ID ADG11172 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1204
ID ADG11951 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1205
ID ADF94508 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1206
ID ADG06604 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1207
ID ADH38948 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1208
ID ADG34038 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1209
ID ADI33508 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1210
ID ADH69602 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1211
ID ADI29763 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1212
ID ADM27160 standard; protein; 572 AA.
DE Novel human secreted and transmembrane protein PRO9925.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1213
ID ADK66518 standard; protein; 572 AA.
DE Human PRO polypeptide #21.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.6e+02;
RESULT 1214
ID ABB91918 standard; protein; 627 AA.
DE Herbicidally active polypeptide SEQ ID NO 1129.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 5; Length 627;
Best Local Similarity 24.7%; Pred. No. 1.8e+02;
RESULT 1215
ID ABU04619 standard; protein; 668 AA.
DE Human expressed protein tag (EPT) #1285.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 668;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1216
ID ADQ39384 standard; protein; 668 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 71; DB 8; Length 668;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1217
ID ABU04602 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1268.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 676;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1218
ID ABU04652 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1318.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 676;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1219
ID ABU24176 standard; protein; 685 AA.

DE Protein encoded by Prokaryotic essential gene #9703.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 71; DB 6; Length 685;
Best Local Similarity 27.8%; Pred. No. 2.1e+02;
RESULT 1220
ID AAY81806 standard; protein; 686 AA.
DE Human mahogany protein sequence #1.
PN WO200005373-A2.
PD 03-FEB-2000.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.4%; Score 71; DB 3; Length 686;
Best Local Similarity 19.1%; Pred. No. 2.1e+02;
RESULT 1221
ID ABU04621 standard; protein; 691 AA.
DE Human expressed protein tag (EPT) #1287.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 691;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1222
ID ADQ39390 standard; protein; 691 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 71; DB 8; Length 691;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1223
ID ABU56470 standard; protein; 699 AA.
DE Lung cancer-associated polypeptide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.4%; Score 71; DB 6; Length 699;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1224
ID ABU04647 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1313.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 699;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1225
ID ABU04614 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1280.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 699;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1226
ID ABU04608 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1274.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 699;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1227
ID ADD90596 standard; protein; 699 AA.
DE Human CD44v glycoprotein SEQ ID NO:6.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 6.4%; Score 71; DB 7; Length 699;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1228
ID AAY97579 standard; protein; 700 AA.
DE Human CD44 splice variant (RA-CD44) protein sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Query Match 6.4%; Score 71; DB 4; Length 700;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1229
ID ABU04640 standard; protein; 700 AA.
DE Human expressed protein tag (EPT) #1306.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 700;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1230
ID ADD90594 standard; protein; 700 AA.
DE Human CD44v glycoprotein SEQ ID NO:4.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 6.4%; Score 71; DB 7; Length 700;
Best Local Similarity 20.2%; Pred. No. 2.1e+02;
RESULT 1231
ID ABU04604 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1270.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 719;
Best Local Similarity 20.2%; Pred. No. 2.2e+02;
RESULT 1232
ID ABU04650 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1316.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 719;
Best Local Similarity 20.2%; Pred. No. 2.2e+02;
RESULT 1233
ID ABG17071 standard; protein; 742 AA.
DE Novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 71; DB 4; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1234
ID ABU04653 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1319.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1235
ID ABU04620 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1286.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1236
ID ABU04645 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1311.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1237
ID ABU04616 standard; protein; 742 AA.

DE Human expressed protein tag (EPT) #1282.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.4%; Score 71; DB 6; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1238
ID ADN95511 standard; protein; 742 AA.
DE Human BEC/LEC-related protein sequence SeqID434.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 6.4%; Score 71; DB 7; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1239
ID ADP65295 standard; protein; 742 AA.
DE Human CD44 antigen (homing function and Indian blood group system), CD44.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 6.4%; Score 71; DB 7; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1240
ID ADL61252 standard; protein; 742 AA.
DE Human protein tyrosine kinase biomarker CD44 antigen protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.4%; Score 71; DB 8; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1241
ID ADL93506 standard; protein; 742 AA.
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 6.4%; Score 71; DB 8; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1242
ID ADO55181 standard; protein; 742 AA.
DE Protein #83 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 6.4%; Score 71; DB 8; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1243
ID ADQ39383 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 71; DB 8; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1244
ID ADQ39391 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 71; DB 8; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1245
ID ADQ39386 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 71; DB 8; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1246
ID ADR67253 standard; protein; 742 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 6.4%; Score 71; DB 8; Length 742;
Best Local Similarity 20.2%; Pred. No. 2.3e+02;
RESULT 1247
ID AAU09864 standard; protein; 801 AA.
DE Novel human secreted protein #5.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.4%; Score 71; DB 5; Length 801;
Best Local Similarity 31.8%; Pred. No. 2.6e+02;
RESULT 1248
ID ADJ70665 standard; protein; 801 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2471.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 6.4%; Score 71; DB 7; Length 801;
Best Local Similarity 31.8%; Pred. No. 2.6e+02;
RESULT 1249
ID AAE02339 standard; protein; 873 AA.
DE Drosophila melanogaster chloride channel (dmCLC) protein.
PN WO200138359-A2.
PD 31-MAY-2001.
PA (GENO-) GENOPTERA LLC.
Query Match 6.4%; Score 71; DB 4; Length 873;
Best Local Similarity 20.9%; Pred. No. 2.9e+02;
RESULT 1250
ID ADJ83142 standard; protein; 1161 AA.
DE Murine integrin alpha 7 protein - SEQ ID 133.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 6.4%; Score 71; DB 7; Length 1161;
Best Local Similarity 22.3%; Pred. No. 4.3e+02;
RESULT 1251
ID ADL16198 standard; protein; 1238 AA.
DE Mouse protein tyrosine phosphatase #4.

PN WO2003068984-A2.
PD 21-AUG-2003.
PA (COLD-) COLD SPRING HARBOR LAB.
PA (CEPT-) CEPTYR INC.
Query Match 6.4%; Score 71; DB 7; Length 1238;
Best Local Similarity 25.6%; Pred. No. 4.7e+02;
RESULT 1252
ID AAY70690 standard; protein; 1355 AA.
DE Human membrane attractin-1.
PN WO200015651-A1.
PD 23-MAR-2000.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 6.4%; Score 71; DB 3; Length 1355;
Best Local Similarity 19.1%; Pred. No. 5.4e+02;
RESULT 1253
ID ADI21666 standard; protein; 1370 AA.
DE Novel human polypeptide #145.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 71; DB 7; Length 1370;
Best Local Similarity 18.3%; Pred. No. 5.5e+02;
RESULT 1254
ID AAY70691 standard; protein; 1429 AA.
DE Human membrane attractin-2.
PN WO200015651-A1.
PD 23-MAR-2000.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 6.4%; Score 71; DB 3; Length 1429;
Best Local Similarity 19.1%; Pred. No. 5.8e+02;
RESULT 1255
ID ABG08472 standard; protein; 1429 AA.
DE Novel human diagnostic protein #8463.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 71; DB 4; Length 1429;
Best Local Similarity 19.1%; Pred. No. 5.8e+02;
RESULT 1256
ID ADN39110 standard; protein; 1460 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:428.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.4%; Score 71; DB 7; Length 1460;
Best Local Similarity 18.3%; Pred. No. 6e+02;
RESULT 1257
ID ABB57380 standard; protein; 1495 AA.
DE Rat mucocardial cell proliferation associated polypeptide SEQ ID NO 12.
PN WO200183705-A1.
PD 08-NOV-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.4%; Score 71; DB 5; Length 1495;
Best Local Similarity 31.8%; Pred. No. 6.2e+02;
RESULT 1258
ID ADE57115 standard; protein; 1496 AA.
DE Rat Protein L19180, SEQ ID NO 2975.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 7; Length 1496;
Best Local Similarity 31.8%; Pred. No. 6.2e+02;
RESULT 1259
ID ADE57119 standard; protein; 1496 AA.
DE Rat Protein L19180, SEQ ID NO 2979.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 7; Length 1496;
Best Local Similarity 31.8%; Pred. No. 6.2e+02;
RESULT 1260
ID ADD47013 standard; protein; 1496 AA.
DE Rat Protein L19180, SEQ ID NO 12699.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 7; Length 1496;
Best Local Similarity 31.8%; Pred. No. 6.2e+02;
RESULT 1261
ID ADD47017 standard; protein; 1496 AA.
DE Rat Protein L19180, SEQ ID NO 12703.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 7; Length 1496;
Best Local Similarity 31.8%; Pred. No. 6.2e+02;
RESULT 1262
ID AAR72858 standard; protein; 1501 AA.
DE Rat receptor type-protein tyrosine phophatase sigma.
PN WO9509656-A1.
PD 13-APR-1995.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 6.4%; Score 71; DB 2; Length 1501;
Best Local Similarity 31.8%; Pred. No. 6.2e+02;
RESULT 1263
ID ADI21202 standard; protein; 1538 AA.
DE Novel human protein #177.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 71; DB 7; Length 1538;
Best Local Similarity 18.3%; Pred. No. 6.4e+02;
RESULT 1264
ID ADD46989 standard; protein; 1863 AA.
DE Rat Protein AAC37656, SEQ ID NO 12675.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 7; Length 1863;
Best Local Similarity 31.8%; Pred. No. 8.4e+02;
RESULT 1265
ID ABB57100 standard; protein; 1904 AA.
DE Mouse ischaemic condition related protein sequence SEQ ID NO:224.
PN WO200188188-A2.
PD 22-NOV-2001.
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
Query Match 6.4%; Score 71; DB 5; Length 1904;
Best Local Similarity 31.8%; Pred. No. 8.6e+02;
RESULT 1266
ID AAR71726 standard; protein; 1911 AA.
DE Human PTP-OB.
PN WO9507935-A1.
PD 23-MAR-1995.
PA (MERI) MERCK & CO INC.
Query Match 6.4%; Score 71; DB 2; Length 1911;
Best Local Similarity 31.8%; Pred. No. 8.7e+02;
RESULT 1267
ID AAW27225 standard; protein; 1911 AA.
DE Human protein tyrosine phosphatase PTP-OB.
PN US5658756-A.
PD 19-AUG-1997.
PA (MERI) MERCK & CO INC.
Query Match 6.4%; Score 71; DB 2; Length 1911;
Best Local Similarity 31.8%; Pred. No. 8.7e+02;
RESULT 1268
ID AAW94027 standard; protein; 1911 AA.
DE Human protein tyrosine phosphatase (PTP-OB).
PN US5866397-A.
PD 02-FEB-1999.
PA (MERI) MERCK & CO INC.
Query Match 6.4%; Score 71; DB 2; Length 1911;

Best Local Similarity 31.8%; Pred. No. 8.7e+02;
RESULT 1269
ID AAU01459 standard; protein; 1911 AA.
DE Human protein tyrosine phosphatase, PTP-OB, amino acid sequence.
PN US6214564-B1.
PD 10-APR-2001.
PA (MERI) MERCK & CO INC.
Query Match 6.4%; Score 71; DB 4; Length 1911;
Best Local Similarity 31.8%; Pred. No. 8.7e+02;
RESULT 1270
ID ADD18742 standard; protein; 1948 AA.
DE Human disease related protein SeqID173.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 6.4%; Score 71; DB 7; Length 1948;
Best Local Similarity 31.8%; Pred. No. 8.9e+02;
RESULT 1271
ID ADE57117 standard; protein; 1949 AA.
DE Human Protein U35234, SEQ ID NO 2977.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 7; Length 1949;
Best Local Similarity 31.8%; Pred. No. 8.9e+02;
RESULT 1272
ID ADE57121 standard; protein; 1949 AA.
DE Human Protein U35234, SEQ ID NO 2981.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 7; Length 1949;
Best Local Similarity 31.8%; Pred. No. 8.9e+02;
RESULT 1273
ID ADD47019 standard; protein; 1949 AA.
DE Human Protein U35234, SEQ ID NO 12705.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 7; Length 1949;
Best Local Similarity 31.8%; Pred. No. 8.9e+02;
RESULT 1274
ID ADD47015 standard; protein; 1949 AA.
DE Human Protein U35234, SEQ ID NO 12701.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 71; DB 7; Length 1949;
Best Local Similarity 31.8%; Pred. No. 8.9e+02;
RESULT 1275
ID ADP23496 standard; protein; 2000 AA.
DE PRO polypeptide SEQ ID NO:674.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.4%; Score 71; DB 8; Length 2000;
Best Local Similarity 25.6%; Pred. No. 9.3e+02;
RESULT 1276
ID AAY81807 standard; protein; 2787 AA.
DE Human mahogany protein sequence #2.
PN WO200005373-A2.
PD 03-FEB-2000.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.4%; Score 71; DB 3; Length 2787;
Best Local Similarity 19.1%; Pred. No. 1.5e+03;
RESULT 1277
ID ADN73145 standard; protein; 5155 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 1040.
PN WO2004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDESIGN NV.
Query Match 6.4%; Score 71; DB 8; Length 5155;
Best Local Similarity 18.4%; Pred. No. 3.5e+03;
RESULT 1278
ID AAM38777 standard; protein; 138 AA.
DE Human polypeptide SEQ ID NO 1922.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 70.5; DB 4; Length 138;
Best Local Similarity 22.3%; Pred. No. 25;
RESULT 1279
ID AAU14339 standard; protein; 138 AA.
DE Human novel protein #210.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 70.5; DB 4; Length 138;
Best Local Similarity 22.3%; Pred. No. 25;
RESULT 1280
ID AAM40563 standard; protein; 155 AA.
DE Human polypeptide SEQ ID NO 5494.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 70.5; DB 4; Length 155;
Best Local Similarity 22.3%; Pred. No. 29;
RESULT 1281
ID ABB90250 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 2626.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 70.5; DB 5; Length 258;
Best Local Similarity 24.9%; Pred. No. 60;
RESULT 1282
ID ABP68491 standard; protein; 303 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:174.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.4%; Score 70.5; DB 5; Length 303;
Best Local Similarity 24.6%; Pred. No. 75;
RESULT 1283
ID ADM18809 standard; protein; 303 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:174.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.4%; Score 70.5; DB 8; Length 303;
Best Local Similarity 24.6%; Pred. No. 75;
RESULT 1284
ID ADR41425 standard; protein; 305 AA.
DE Human CD-like molecule HOUCD83, SEQ ID NO:224.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 70.5; DB 5; Length 305;
Best Local Similarity 24.9%; Pred. No. 76;
RESULT 1285
ID AAY09188 standard; protein; 516 AA.
DE Soybean cytochrome P450 enzyme, CYP83D1.
PN WO9919493-A2.
PD 22-APR-1999.
PA (UYNC-) UNIV NORTH CAROLINA STATE.
Query Match 6.4%; Score 70.5; DB 2; Length 516;
Best Local Similarity 23.2%; Pred. No. 1.6e+02;
RESULT 1286
ID ABB58504 standard; protein; 518 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2304.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 70.5; DB 4; Length 518;
Best Local Similarity 24.2%; Pred. No. 1.6e+02;
RESULT 1287
ID AAM39143 standard; protein; 555 AA.
DE Human polypeptide SEQ ID NO 2288.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 70.5; DB 4; Length 555;
Best Local Similarity 24.9%; Pred. No. 1.8e+02;
RESULT 1288
ID ABP69054 standard; protein; 801 AA.
DE Human polypeptide SEQ ID NO 1101.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 70.5; DB 5; Length 801;
Best Local Similarity 32.0%; Pred. No. 2.9e+02;
RESULT 1289
ID AAY72616 standard; protein; 854 AA.
DE Carassius auratus full-length CaSR-like protein #3.
PN WO200105833-A1.
PD 25-JAN-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.4%; Score 70.5; DB 4; Length 854;
Best Local Similarity 27.5%; Pred. No. 3.2e+02;
RESULT 1290
ID ABB93062 standard; protein; 900 AA.
DE Herbicidally active polypeptide SEQ ID NO 2273.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 70.5; DB 5; Length 900;
Best Local Similarity 26.4%; Pred. No. 3.4e+02;
RESULT 1291
ID ABG21347 standard; protein; 1131 AA.
DE Novel human diagnostic protein #21338.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 70.5; DB 4; Length 1131;
Best Local Similarity 22.0%; Pred. No. 4.7e+02;
RESULT 1292
ID ABG24027 standard; protein; 1142 AA.
DE Novel human diagnostic protein #24018.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 70.5; DB 4; Length 1142;
Best Local Similarity 22.0%; Pred. No. 4.8e+02;
RESULT 1293
ID ABB71304 standard; protein; 1171 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40704.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 70.5; DB 4; Length 1171;
Best Local Similarity 18.5%; Pred. No. 5e+02;
RESULT 1294
ID ADS43524 standard; protein; 1173 AA.
DE Bacterial polypeptide #21954.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.4%; Score 70.5; DB 8; Length 1173;
Best Local Similarity 20.1%; Pred. No. 5e+02;
RESULT 1295
ID AAY07729 standard; protein; 1183 AA.
DE Armenian hamster alpha-2 integrin subunit protein.
PN WO9916465-A1.
PD 08-APR-1999.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA (SENG/) SENGER D R.
PA (DETM/) DETMAR M.
PA (CLAF/) CLAFFEY K P.
Query Match 6.4%; Score 70.5; DB 2; Length 1183;
Best Local Similarity 23.5%; Pred. No. 5e+02;
RESULT 1296
ID ABR52622 standard; protein; 2000 AA.
DE Protein sequence #SEQ ID 109.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 6.4%; Score 70.5; DB 6; Length 2000;
Best Local Similarity 21.6%; Pred. No. 1.1e+03;
RESULT 1297
ID ADK62602 standard; protein; 2000 AA.
DE Disease treating protein complex-derived protein #427.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 6.4%; Score 70.5; DB 7; Length 2000;
Best Local Similarity 21.6%; Pred. No. 1.1e+03;
RESULT 1298
ID ABR33444 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1797.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 70; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3;
RESULT 1299
ID ABR33416 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1769.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 70; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3;
RESULT 1300
ID ABR33322 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1675.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 70; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3;
RESULT 1301
ID ABR33294 standard; peptide; 15 AA.
DE Human cancer-related protein 156P5C12 HLA peptide #1647.
PN WO200283921-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.4%; Score 70; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3;
RESULT 1302
ID AAG74274 standard; protein; 176 AA.
DE Human colon cancer antigen protein SEQ ID NO:5038.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.4%; Score 70; DB 4; Length 176;
Best Local Similarity 22.1%; Pred. No. 40;
RESULT 1303
ID ABP64767 standard; protein; 216 AA.
DE Human protein SEQ ID 427.
PN WO200259260-A2.
PD 01-AUG-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 70; DB 5; Length 216;
Best Local Similarity 19.3%; Pred. No. 53;

RESULT 1304
ID ABU41212 standard; protein; 221 AA.
DE Protein encoded by Prokaryotic essential gene #26739.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 70; DB 6; Length 221;
Best Local Similarity 28.3%; Pred. No. 55;
RESULT 1305
ID ADQ59457 standard; protein; 298 AA.
DE Human cancer-associated (CA) protein sequence SEQ ID NO:93.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 6.4%; Score 70; DB 8; Length 298;
Best Local Similarity 19.5%; Pred. No. 83;
RESULT 1306
ID ABP29640 standard; protein; 341 AA.
DE Streptococcus polypeptide SEQ ID NO 8456.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.4%; Score 70; DB 5; Length 341;
Best Local Similarity 26.1%; Pred. No. 1e+02;
RESULT 1307
ID ABU46900 standard; protein; 341 AA.
DE Protein encoded by Prokaryotic essential gene #32427.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 70; DB 6; Length 341;
Best Local Similarity 26.1%; Pred. No. 1e+02;
RESULT 1308
ID ADQ65785 standard; protein; 396 AA.
DE Novel human protein sequence #758.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 70; DB 8; Length 396;
Best Local Similarity 23.5%; Pred. No. 1.2e+02;
RESULT 1309
ID ABB54978 standard; protein; 544 AA.
DE Lactococcus lactis protein uxuB.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.4%; Score 70; DB 5; Length 544;
Best Local Similarity 25.7%; Pred. No. 1.9e+02;
RESULT 1310
ID ABG08976 standard; protein; 563 AA.
DE Novel human diagnostic protein #8967.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 70; DB 4; Length 563;
Best Local Similarity 20.8%; Pred. No. 2e+02;
RESULT 1311
ID ABB65057 standard; protein; 678 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21963.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 70; DB 4; Length 678;
Best Local Similarity 24.6%; Pred. No. 2.6e+02;
RESULT 1312
ID ABB58451 standard; protein; 738 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2145.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 70; DB 4; Length 738;
Best Local Similarity 22.3%; Pred. No. 3e+02;
RESULT 1313
ID AAU38924 standard; protein; 738 AA.
DE Drosophila G-protein coupled receptor, GCPR #2.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.4%; Score 70; DB 4; Length 738;
Best Local Similarity 22.3%; Pred. No. 3e+02;
RESULT 1314
ID ADC35754 standard; protein; 738 AA.
DE Drosophila G protein coupled receptor seq id 4.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match 6.4%; Score 70; DB 7; Length 738;
Best Local Similarity 22.3%; Pred. No. 3e+02;
RESULT 1315
ID ADN96168 standard; protein; 863 AA.
DE Human NOVX polypeptide #111.
PN US2004067490-A1.
PD 08-APR-2004.
PA (ZHON/) ZHONG M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (SPYT/) SPYTEK K A.
PA (KEKU/) KEKUDA R.
PA (TAUP/) TAUPIER R J.
PA (ANDE/) ANDERSON D W.
PA (VERN/) VERNET C A M.
PA (CATT/) CATTERTON E.
PA (MILL/) MILLER C E.
PA (SHEN/) SHENOY S G.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (TCHE/) TCHERNEV V T.
PA (PADI/) PADIGARU M.
PA (GUSE/) GUSEV V Y.
PA (MALY/) MALYANKAR U M.
PA (BURG/) BURGESS C E.
PA (GERL/) GERLACH V.
PA (CASM/) CASMAN S J.
PA (RIEG/) RIEGER D K.
PA (GROS/) GROSSE W M.
PA (SMIT/) SMITHSON G.
PA (PEYM/) PEYMAN J A.
PA (STAR/) STARLING G.
PA (ROTH/) ROTHENBERG M E.
PA (LARO/) LAROCHELLE W J.
PA (SHIM/) SHIMKETS R A.
PA (CRAB/) CRABTREE J.
PA (RAST/) RASTELLI L.
PA (VOSS/) VOSS E Z.
PA (BOLD/) BOLDOG F L.
PA (EDIN/) EDINGER S R.
PA (MILL/) MILLET I.
PA (MACD/) MACDOUGALL J R.
PA (ELLE/) ELLERMAN K.
PA (CHAP/) CHAPOVAL A.
Query Match 6.4%; Score 70; DB 8; Length 863;
Best Local Similarity 22.9%; Pred. No. 3.7e+02;
RESULT 1316
ID AAY49554 standard; protein; 1039 AA.
DE Human platelet membrane glycoprotein IIb protein sequence.
PN WO9950454-A2.
PD 07-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 6.4%; Score 70; DB 2; Length 1039;
Best Local Similarity 20.2%; Pred. No. 4.8e+02;
RESULT 1317
ID AAY92445 standard; protein; 1039 AA.
DE Wild type human GPIIb, form Bak-a.
PN WO200020634-A1.
PD 13-APR-2000.

PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.4%; Score 70; DB 3; Length 1039;
Best Local Similarity 20.2%; Pred. No. 4.8e+02;
RESULT 1318
ID AAY92446 standard; protein; 1039 AA.
DE Variant human GPIIb, form Bak-b.
PN WO200020634-A1.
PD 13-APR-2000.
PA (NOVA-) NOVA MOLECULAR INC.
Query Match 6.4%; Score 70; DB 3; Length 1039;
Best Local Similarity 20.2%; Pred. No. 4.8e+02;
RESULT 1319
ID ADD45808 standard; protein; 1039 AA.
DE Human Protein P08514, SEQ ID NO 11477.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 70; DB 7; Length 1039;
Best Local Similarity 20.2%; Pred. No. 4.8e+02;
RESULT 1320
ID ADE60212 standard; protein; 1039 AA.
DE Human Protein P08514, SEQ ID NO 6118.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 70; DB 7; Length 1039;
Best Local Similarity 20.2%; Pred. No. 4.8e+02;
RESULT 1321
ID ADI22190 standard; protein; 1039 AA.
DE Human platelet membrane glycoprotein IIb protein SEQ:153.
PN WO2004005890-A2.
PD 15-JAN-2004.
PA (UYPE-) UNIV PENNSYLVANIA.
Query Match 6.4%; Score 70; DB 8; Length 1039;
Best Local Similarity 20.2%; Pred. No. 4.8e+02;
RESULT 1322
ID ADM99591 standard; protein; 1039 AA.
DE Human integrin alphaIIb subunit precursor protein.
PN WO2004007530-A2.
PD 22-JAN-2004.
PA (BLOO-) CENT BLOOD RES INC.
Query Match 6.4%; Score 70; DB 8; Length 1039;
Best Local Similarity 20.2%; Pred. No. 4.8e+02;
RESULT 1323
ID ADP12420 standard; protein; 1039 AA.
DE Protein encoded by mRNA of the invention #30.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.4%; Score 70; DB 8; Length 1039;
Best Local Similarity 20.2%; Pred. No. 4.8e+02;
RESULT 1324
ID ADP74025 standard; protein; 1178 AA.
DE Murine CD49b protein, a target of Th1 helper T cells Seq 15.
PN JP2004147534-A.
PD 27-MAY-2004.
PA (NISH/) NISHIMURA T.
PA (TORA) TORAY IND INC.
Query Match 6.4%; Score 70; DB 8; Length 1178;
Best Local Similarity 23.8%; Pred. No. 5.7e+02;
RESULT 1325
ID ABG30775 standard; protein; 214 AA.
DE Human vesicular membrane-spanning protein VIP36-23.54.
PN CN1341651-A.
PD 27-MAR-2002.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 6.3%; Score 69.5; DB 5; Length 214;
Best Local Similarity 21.7%; Pred. No. 60;
RESULT 1326
ID ADR09157 standard; protein; 215 AA.
DE Human protein useful for treating neurological disease Seq 2663.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.3%; Score 69.5; DB 8; Length 215;
Best Local Similarity 24.7%; Pred. No. 60;
RESULT 1327
ID AAU75545 standard; protein; 270 AA.
DE Mouse B7-like protein, B7-L_m2.
PN WO200200710-A2.
PD 03-JAN-2002.
PA (AMGE-) AMGEN INC.
Query Match 6.3%; Score 69.5; DB 5; Length 270;
Best Local Similarity 24.4%; Pred. No. 83;
RESULT 1328
ID ADJ94243 standard; protein; 274 AA.
DE Mouse IPC marker Ly-49Q, SEQ ID 2.
PN WO2004013325-A1.
PD 12-FEB-2004.
PA (GINK-) GINKGO BIOMEDICAL RES INST CO LTD.
Query Match 6.3%; Score 69.5; DB 8; Length 274;
Best Local Similarity 25.3%; Pred. No. 84;
RESULT 1329
ID AAU03560 standard; protein; 290 AA.
DE Mouse immunoregulatory protein B7-H1.
PN WO200139722-A2.
PD 07-JUN-2001.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 6.3%; Score 69.5; DB 4; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1330
ID AAY72646 standard; protein; 290 AA.
DE Murine B7-4 protein.
PN WO200114556-A1.
PD 01-MAR-2001.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 6.3%; Score 69.5; DB 4; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1331
ID AAY72678 standard; protein; 290 AA.
DE Murine B7-4 protein.
PN WO200114557-A1.
PD 01-MAR-2001.
PA (DAND) DANA FARBER CANCER INST INC.
PA (GEMY) GENETICS INST INC.
Query Match 6.3%; Score 69.5; DB 4; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1332
ID AAE16963 standard; protein; 290 AA.
DE Mouse PD-1 ligand (PD-L1).
PN WO200200730-A2.
PD 03-JAN-2002.
PA (GEMY) GENETICS INST INC.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 6.3%; Score 69.5; DB 5; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1333
ID AAO15819 standard; protein; 290 AA.
DE Murine B7H1 protein.
PN US2002106730-A1.
PD 08-AUG-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.3%; Score 69.5; DB 5; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1334
ID AAE33392 standard; protein; 290 AA.
DE Murine B7-4 protein.
PN WO200279499-A1.
PD 10-OCT-2002.
PA (AMHP) WYETH.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 6.3%; Score 69.5; DB 6; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1335

ID ABJ18520 standard; protein; 290 AA.
DE Murine PD-L1 protein.
PN WO200278731-A1.
PD 10-OCT-2002.
PA (AMHP) WYETH.
Query Match 6.3%; Score 69.5; DB 6; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1336
ID ABG75660 standard; protein; 290 AA.
DE Murine PD-L1 polypeptide.
PN US2002164600-A1.
PD 07-NOV-2002.
PA (FREE/) FREEMAN G.
PA (CHER/) CHERNOVA I.
PA (CHER/) CHERNOVA T.
PA (MALE/) MALENKOVICH N.
PA (WOOD/) WOOD C.
Query Match 6.3%; Score 69.5; DB 6; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1337
ID ADJ76248 standard; protein; 290 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1500.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 6.3%; Score 69.5; DB 8; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1338
ID ADQ76324 standard; protein; 290 AA.
DE Murine B7-H1 protein.
PN US2004137577-A1.
PD 15-JUL-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.3%; Score 69.5; DB 8; Length 290;
Best Local Similarity 23.6%; Pred. No. 91;
RESULT 1339
ID ABU01702 standard; protein; 296 AA.
DE S. pneumoniae type 4 strain protein from coding region #1278.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.3%; Score 69.5; DB 6; Length 296;
Best Local Similarity 20.6%; Pred. No. 94;
RESULT 1340
ID ABU46086 standard; protein; 296 AA.
DE Protein encoded by Prokaryotic essential gene #31613.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 69.5; DB 6; Length 296;
Best Local Similarity 20.6%; Pred. No. 94;
RESULT 1341
ID ABP68464 standard; protein; 302 AA.
DE Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:68.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Query Match 6.3%; Score 69.5; DB 5; Length 302;
Best Local Similarity 21.0%; Pred. No. 97;
RESULT 1342
ID ADM18703 standard; protein; 302 AA.
DE Human co-stimulatory molecule protein SEQ ID NO:68.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Query Match 6.3%; Score 69.5; DB 8; Length 302;
Best Local Similarity 21.0%; Pred. No. 97;
RESULT 1343
ID AAM79020 standard; protein; 313 AA.
DE Human protein SEQ ID NO 1682.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 69.5; DB 4; Length 313;
Best Local Similarity 21.7%; Pred. No. 1e+02;
RESULT 1344
ID ABB12008 standard; peptide; 314 AA.
DE Human PRO704 homologue, SEQ ID NO:2378.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 69.5; DB 4; Length 314;
Best Local Similarity 21.7%; Pred. No. 1e+02;
RESULT 1345
ID AAM80004 standard; protein; 314 AA.
DE Human protein SEQ ID NO 3650.
PN WO200157190-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 69.5; DB 4; Length 314;
Best Local Similarity 21.7%; Pred. No. 1e+02;
RESULT 1346
ID AAW67846 standard; protein; 323 AA.
DE Human secreted protein encoded by gene 40 clone HTOEU03.
PN WO9842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.3%; Score 69.5; DB 2; Length 323;
Best Local Similarity 21.7%; Pred. No. 1.1e+02;
RESULT 1347
ID AAY41741 standard; protein; 348 AA.
DE Human PRO704 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 2; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1348
ID AAB44297 standard; protein; 348 AA.
DE Human PRO704 (UNQ368) protein sequence SEQ ID NO:380.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 3; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1349
ID AAB88578 standard; protein; 348 AA.
DE Human hydrophobic domain containing protein clone HP03747 #62.
PN WO200112660-A2.
PD 22-FEB-2001.
PA (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
Query Match 6.3%; Score 69.5; DB 4; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1350
ID AAU29070 standard; protein; 348 AA.
DE Human PRO polypeptide sequence #47.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 4; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1351
ID AAM39973 standard; protein; 348 AA.
DE Human polypeptide SEQ ID NO 3118.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.3%; Score 69.5; DB 4; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1352
ID ABU52663 standard; protein; 348 AA.
DE Intracellular transport and trafficking protein from DKFZphfbr2_23124.
PN WO200112659-A2.
PD 22-FEB-2001.

PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 6.3%; Score 69.5; DB 4; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1353
ID ABB89148 standard; protein; 348 AA.
DE Human polypeptide SEQ ID NO 1524.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.3%; Score 69.5; DB 5; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1354
ID ABU58446 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1355
ID ABU87994 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1356
ID ABU84309 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1357
ID ABR66183 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1358
ID ABR65573 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1359
ID ABU99513 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1360
ID ABU82752 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1361
ID ABU89873 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1362
ID ABR68122 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1363
ID ABU96175 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1364
ID ABU92606 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1365
ID ABO08683 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1366
ID ABO02735 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1367
ID ABR74889 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1368
ID ABR94651 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1369
ID ABO25243 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1370
ID ABU85624 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1371
ID ABU98784 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1372
ID ABU97999 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;

RESULT 1373
ID ABU91705 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1374
ID ABU72249 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1375
ID ABU89398 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1376
ID ABU86239 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1377
ID ABU67452 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1378
ID ABU80480 standard; protein; 348 AA.
DE Human PRO protein #47.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1379
ID ABR99398 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1380
ID ABR98788 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1381
ID ABO16311 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1382
ID ABR92211 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1383
ID ABO18852 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1384
ID ABR78273 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1385
ID ABU85009 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1386
ID ABO00148 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1387
ID ABO11480 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1388
ID ABO02125 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1389
ID ABU88699 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1390
ID ABU83394 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1391
ID ABO06195 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1392
ID ABR59231 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1393

ID ABO09293 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1394
ID ABO19157 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1395
ID ABO11175 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1396
ID ABR66793 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1397
ID ABO16006 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1398
ID ABO13712 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1399
ID ABU84929 standard; protein; 348 AA.
DE Human secreted and transmembrane PRO polypeptide #5.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1400
ID ABU65615 standard; protein; 348 AA.
DE Human secreted/transmembrane protein, SEQ ID 94.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1401
ID ABO07463 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1402
ID ABO03650 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1403
ID ABR67098 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1404
ID ABO15701 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1405
ID ABU55982 standard; protein; 348 AA.
DE Human secreted/transmembrane protein, PRO704.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1406
ID ABU61127 standard; protein; 348 AA.
DE Human PRO704 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1407
ID ABU65310 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1408
ID ABU95255 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1409
ID ABU71158 standard; protein; 348 AA.
DE Human PRO704 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1410
ID ABO07768 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1411
ID ABR70009 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1412
ID ABR69342 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1413
ID ABO01483 standard; protein; 348 AA.

DE Human PRO polypeptide #47.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1414
ID ABU81285 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1415
ID ABR60082 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1416
ID ABR67817 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1417
ID ABR65205 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1418
ID ABR68427 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1419
ID ABR71839 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1420
ID ABU85319 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1421
ID ABU89009 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1422
ID ABU83089 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1423
ID ABU94945 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1424
ID ABU90493 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1425
ID ABU84004 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1426
ID ABU93655 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1427
ID ABR64900 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1428
ID ABR68732 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1429
ID ABO06548 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1430
ID ABR99093 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1431
ID ABU56977 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1432
ID ABU85929 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1433
ID ABU82216 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003036136-A1.
PD 20-FEB-2003.

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  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1434
ID   ABU87227 standard; protein; 348 AA.
DE   Human PRO polypeptide #47.
PN   US2003036138-A1.
PD   20-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1435
ID   ABU83699 standard; protein; 348 AA.
DE   Human secreted/transmembrane protein (PRO) #47.
PN   US2003032109-A1.
PD   13-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1436
ID   ABO08073 standard; protein; 348 AA.
DE   Human PRO polypeptide #47.
PN   US2003040066-A1.
PD   27-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1437
ID   ABU81784 standard; protein; 348 AA.
DE   Novel human secreted and transmembrane protein PRO704.
PN   US2003032104-A1.
PD   13-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1438
ID   ABU65948 standard; protein; 348 AA.
DE   Novel human secreted and transmembrane protein PRO704.
PN   US2003036157-A1.
PD   20-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1439
ID   ABR59777 standard; protein; 348 AA.
DE   Human secreted polypeptide PRO704, SEQ ID NO:94.
PN   US2003032120-A1.
PD   13-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1440
ID   ABU93965 standard; protein; 348 AA.
DE   Novel human secreted and transmembrane protein PRO704.
PN   US2003036155-A1.
PD   20-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1441
ID   ABU80396 standard; protein; 348 AA.
DE   Human secreted/transmembrane protein PRO704.
PN   US2003004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1442
ID   ABU99818 standard; protein; 348 AA.
DE   Novel human secreted and transmembrane protein PRO704.
PN   US2003022296-A1.
PD   30-JAN-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1443
ID   ABR66488 standard; protein; 348 AA.
DE   Human secreted polypeptide PRO704, SEQ ID NO:94.
PN   US2003027281-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1444
ID   ABR90906 standard; protein; 348 AA.
DE   Human secreted polypeptide PRO704, SEQ ID NO:94.
PN   US2003040058-A1.
PD   27-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1445
ID   ABU94333 standard; protein; 348 AA.
DE   Human PRO polypeptide #47.
PN   US2003017540-A1.
PD   23-JAN-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1446
ID   ABU79215 standard; protein; 348 AA.
DE   Human PRO polypeptide #47.
PN   US2003032106-A1.
PD   13-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1447
ID   ABU86544 standard; protein; 348 AA.
DE   Human secreted/transmembrane protein (PRO) #47.
PN   US2003032129-A1.
PD   13-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1448
ID   ABU86849 standard; protein; 348 AA.
DE   Novel human secreted and transmembrane protein PRO704.
PN   US2003032131-A1.
PD   13-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1449
ID   ABU94638 standard; protein; 348 AA.
DE   Human PRO polypeptide #47.
PN   US2003032103-A1.
PD   13-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1450
ID   ABO04565 standard; protein; 348 AA.
DE   Human PRO polypeptide #47.
PN   US2003032107-A1.
PD   13-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1451
ID   ABR70314 standard; protein; 348 AA.
DE   Human secreted polypeptide PRO704, SEQ ID NO:94.
PN   US2003032139-A1.
PD   13-FEB-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1452
ID   ABU98479 standard; protein; 348 AA.
DE   Human PRO polypeptide #47.
PN   US2003022301-A1.
PD   30-JAN-2003.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1453
ID   ABR65878 standard; protein; 348 AA.
DE   Human secreted polypeptide PRO704, SEQ ID NO:94.
PN   US2003036165-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             6.3%;  Score 69.5;  DB 6;  Length 348;
  Best Local Similarity   21.7%;  Pred. No. 1.2e+02;
RESULT 1454
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ID ABR64595 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1455
ID ABU79520 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1456
ID ABU92911 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1457
ID ABU95870 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1458
ID ABU91090 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1459
ID ABU90183 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1460
ID ABO09598 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1461
ID ABO10870 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1462
ID ABR70924 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1463
ID ABU87532 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1464
ID ABU91400 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1465
ID ABU84614 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1466
ID ABR69704 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1467
ID ABU80081 standard; protein; 348 AA.
DE Human PRO protein #47.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1468
ID ABU93350 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1469
ID ABO09903 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1470
ID ABO08988 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1471
ID ABU10556 standard; protein; 348 AA.
DE Human secreted/transmembrane protein #47.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1472
ID ABU95565 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1473
ID ABU96774 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1474
ID ABR70619 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1475
ID ABO04970 standard; protein; 348 AA.
DE Novel human secreted and transmembrane protein PRO704.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1476
ID ABO08378 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1477
ID ABO05585 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1478
ID ABR73974 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1479
ID ABR95566 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1480
ID ABR80863 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1481
ID ABR81168 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1482
ID ABM00864 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1483
ID ABR88466 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1484
ID ABM77287 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1485
ID ABO28771 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1486
ID ABO31516 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1487
ID ABM07933 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1488
ID ABO40413 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1489
ID ABO35838 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1490
ID ABO43977 standard; protein; 348 AA.
DE Human PRO polypeptide #47.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1491
ID ADA77846 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1492
ID ABM24772 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1493
ID ABO03040 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003036131-A1.

PD 20-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1494
ID ABR90296 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1495
ID ABM17210 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1496
ID ABR94956 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1497
ID ABR95261 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1498
ID ABO21499 standard; protein; 348 AA.
DE Human secreted/transmembrane protein (PRO) #47.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1499
ID ABR97763 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;
RESULT 1500
ID ABR87551 standard; protein; 348 AA.
DE Human secreted polypeptide PRO704, SEQ ID NO:94.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.3%; Score 69.5; DB 6; Length 348;
Best Local Similarity 21.7%; Pred. No. 1.2e+02;

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